

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 21:46:23 ; Search time 138.474 Seconds
(without alignments)
463.258 Million cell updates/sec

Title: US-10-623-189-1

Perfect score: 736

Sequence: 1 VPQKVQDRTKLIKTIIVTR.....SRQGSIQDMLWQLDLSPGC 146

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 43937871 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq_21:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*
- 9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	736	100.0	146	2	AAW00013	Aaw00013 Acid stab
2	736	100.0	146	2	AAR99490	Aar99490 Chimeric
3	736	100.0	146	2	AAW00539	Aaw00539 Human mat
4	736	100.0	146	2	AAW30892	Aaw30892 Synthetic
5	736	100.0	146	2	AAW34482	Aaw34482 Human obe
6	736	100.0	146	2	AAW10151	Aaw10151 Properly
7	736	100.0	146	2	AAW22901	Aaw22901 Biologica
8	736	100.0	146	2	AAW30791	Aaw30791 Obesity p
9	736	100.0	146	2	AAW26194	Aaw26194 Obesity p
10	736	100.0	146	2	AAW34483	Aaw34483 Human obe
11	736	100.0	146	2	AAW32575	Aaw32575 Anti obes
12	736	100.0	146	2	AAW34489	Aaw34489 Obesity p
13	736	100.0	146	2	AAW69682	Aaw69682 Human obe
14	736	100.0	146	2	AAW53342	Aaw53342 Obesity p
15	736	100.0	146	2	AAW43311	Aaw43311 Human lep
16	736	100.0	146	2	AAW06102	Aaw06102 Human obe
17	736	100.0	146	3	AAW92712	Aay92712 Mature le
18	736	100.0	146	3	AAW82111	Aay82111 Mature hu
19	736	100.0	146	3	AAW80260	Aay80260 Human mat
20	736	100.0	146	3	AAW83768	Aay83768 Human OB
21	736	100.0	146	3	AAW97871	Aay97871 Mature wi
22	736	100.0	146	3	AAW95786	Aay95786 Mature re
23	736	100.0	146	3	AAW95531	Aay95531 Human mat
24	736	100.0	146	3	AAW14265	Aab14265 Mature hu

25	736	100.0	146	4	AAB70130	Aab70130 Mature hu
26	736	100.0	146	5	AAE23614	Aae23614 Human lep
27	736	100.0	146	5	ABG32264	Abg32264 Recombina
28	736	100.0	146	5	ABP63579	Abp63579 Human obe
29	736	100.0	146	5	ADG65529	Adg65529 Human lep
30	736	100.0	146	5	ABR57162	AbR57162 Recombina
31	736	100.0	146	7	ADC06694	Adc06694 Leptin ta
32	736	100.0	146	7	ADD26675	Add26675 Human adi
33	736	100.0	146	7	ADD71107	Add71107 Human lep
34	736	100.0	146	8	ADL80474	Adl80474 Mature hu
35	736	100.0	146	8	ADL88877	Adl88877 Human cyt
36	736	100.0	146	9	ADV90297	Adv90297 Protease-
37	736	100.0	146	9	ADW96956	Adw96956 Human wil
38	736	100.0	147	2	AAW34394	Aaw34394 Human met
39	736	100.0	147	2	AAW27167	Aaw27167 Human rec
40	736	100.0	147	2	AAW53328	Aaw53328 Human obe
41	736	100.0	147	2	AAW43314	Aay43314 Human lep
42	736	100.0	147	3	AAW92261	Aay92261 Mature re
43	736	100.0	148	2	AAW07192	Aaw07192 Human ant
44	736	100.0	148	2	AAW28801	Aaw28801 Human mas
45	736	100.0	148	2	AAW71849	Aaw71849 Obesity p

ALIGNMENTS

RESULT 1
AAW00013
ID AAW00013 standard; protein; 146 AA.
AC AAW00013;
XX
DT 30-SEP-1996 (first entry)
XX
DE Acid stable modified ob protein (Asp22Asn).
XX
KW ob protein; adiposity regulating hormone; mouse; acid stability;
KW adsorption characteristic; obesity; type II diabetes;
KW cardiovascular disease; cancer.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 22
FT Disulfide-bond 96..146
XX
FN EP725078-A1.
XX
PD 07-AUG-1996.
XX
PF 29-JAN-1996; 96EP-00300612.
XX
PR 31-JAN-1995; 95US-00381048.
XX
PR 06-FEB-1995; 95US-00383638.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Basinsky MB, Dimarchi RD, Heath WP, Schoner BE;
XX
DR WPI; 1996-356062/36.
XX
PT Mammalian derived anti-obesity proteins which regulate fat tissue - used
PT for treating obesity and to reduce risk for type II diabetes,
PT cardiovascular disease and cancer.
XX
PS Example 4; Page 19; 42pp; English.
XX
CC This sequence represents a modified ob proteins. ob proteins are thought
CC to be adiposity regulating hormones. This sequence is based on the mouse
CC ob protein sequence. Proteins such as this have improved stability, esp.
CC acid stability, and improved adsorption characteristics compared to the
CC wild type protein disclosed in Yiying Zhang et al, Nature 372: 425-32


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XX 13-SEP-1996 (first entry)
DT Human mature obesity protein.
DE
XX Obesity; mouse; OBP; leptin; hormone; body weight regulation; diabetes;
KW food intake; energy expenditure; high blood pressure; cholesterol; human;
KW gene therapy; antibody; cancer; Kobe beef; Foie gras; immunoassay.
XX Homo sapiens.
OS
XX GB2292382-A.
PN
XX 21-FEB-1996.
PD
XX 17-AUG-1995; 95GB-00016947.
PF
XX 17-AUG-1994; 94US-00292345.
PR 30-NOV-1994; 94US-00347563.
PR 10-MAY-1995; 95US-00438431.
PR 07-JUN-1995; 95US-00483211.
XX (UYRQ ) UNIV ROCKEFELLER.
PA
XX Friedman JM, Zhang Y, Proenca R, Maffei M, Halaas JL, Gajiwala K;
PI Burley SK;
PI
XX WPI; 1996-099009/11.
DR
XX Obesity polypeptide(s) able to modulate body wt. - useful for e.g.
PT reducing wt. in treatment of diabetes, high blood pressure and high
PT cholesterol and for cosmetic reasons.
XX
XX Claim 11; Page 7; 304pp; English.
PS
XX AAW0538-W00541 represent the mature proteins of the murine and human
CC obesity polypeptides (OBP) (full length sequences represented by AAR92719
CC and AAR92720). OBP (also known as leptin) is a hormone involved in the
CC regulation of body weight. This sequence has effects on both food intake
CC and energy expenditure. OBP and its analogues are useful for modifying
CC body weight (optionally combined with known medicaments), for treating
CC diabetes, high blood pressure or high cholesterol. The DNA encoding this
CC sequence (and sequences complementary to it) can be used in gene therapy
CC for modifying body weight. This protein can be used for reducing weight
CC for health or cosmetic reasons in obese humans, or to produce leaner food
CC animals. Antagonists of OBP (including antibodies) are useful for
CC increasing body weight, e.g. for treating weight loss associated with
CC cancer, or for cosmetic reasons in humans, or for production of Kobe beef
CC or Foie gras in domestic animals. OBP antibodies (Ab) can also be used in
CC diagnostic immunoassays for the presence of OBP. The formation of Ab-OBP
CC complexes enables in vitro evaluation of levels of OBP in a sample,
CC especially to detect diseases associated with elevated or decreased
CC levels, and to monitor treatment of these diseases
XX
SQ Sequence 146 AA;
Query Match 100.0%; Score 736; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 9e-73;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60
Db 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60
Qy 61 YQQLTSMPSRNVQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGGVLEASGYS 120
Db 61 YQQLTSMPSRNVQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGGVLEASGYS 120
Qy 121 TEVALSRQGSLOQMLWQLDLSFGC 146
Db 121 TEVALSRQGSLOQMLWQLDLSFGC 146
Query Match 100.0%; Score 736; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 9e-73;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60
Db 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60
Qy 61 YQQLTSMPSRNVQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGGVLEASGYS 120
Db 61 YQQLTSMPSRNVQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGGVLEASGYS 120
Qy 121 TEVALSRQGSLOQMLWQLDLSFGC 146
Db 121 TEVALSRQGSLOQMLWQLDLSFGC 146
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RESULT 4
AAW30892
ID AAW30892 standard; protein; 146 AA.
XX
AC AAW30892;
XX 20-APR-1998 (first entry)
DT Synthetic obesity protein.
DE
XX Obesity protein; sucrose; trehalose; treatment; obesity; diabetes;
KW cardiovascular disease; cancer.
XX Synthetic.
OS
XX EP797999-A2.
PN
XX 01-OCT-1997.
PD
XX 24-MAR-1997; 97EP-00301995.
PF
XX 26-MAR-1996; 96US-0014177P.
PR 05-APR-1996; 96US-0014951P.
XX (ELIL ) LILLY & CO ELI.
PA
XX Beals JM, Edwards MJ, Pikal MJ, Rinella JV;
PI
XX WPI; 1997-472913/44.
DR
XX Pharmaceutical compositions comprising obesity protein - and sucrose
PT and/or trehalose.
PT
XX Claim 2; Page 44; 48pp; English.
PS
XX A novel pharmaceutical composition comprises an obesity protein, e.g. the
CC present sequence, together with sucrose and/or trehalose. The composition
CC can be used to treat obesity and associated disorders, e.g. diabetes,
CC cardiovascular disease and cancer. The composition is stable and easy to
CC manufacture
XX
SQ Sequence 146 AA;
Query Match 100.0%; Score 736; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 9e-73;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60
Db 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60
Qy 61 YQQLTSMPSRNVQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGGVLEASGYS 120
Db 61 YQQLTSMPSRNVQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGGVLEASGYS 120
Qy 121 TEVALSRQGSLOQMLWQLDLSFGC 146
Db 121 TEVALSRQGSLOQMLWQLDLSFGC 146
RESULT 5
AAW34482
ID AAW34482 standard; protein; 146 AA.
XX
AC AAW34482;
XX 17-MAR-1998 (first entry)
DT Human obesity protein.
DE
XX Obesity protein; therapy; obesity associated disorder; human.
KW
XX Homo sapiens.
OS
```

XX EP784979-A2.
 PN
 XX
 PD 23-JUL-1997.
 XX
 PF 17-JAN-1997; 97EP-00300299.
 XX
 PR 19-JAN-1996; 96US-0010229P.
 PR 07-FEB-1996; 96GB-00002408.
 XX
 PA (ELIL) LILLY & CO ELI.
 XX
 XX Beals JM, Dodd SW, Pekar AH;
 XX WPI; 1997-365736/34.
 DR
 XX New obesity protein compositions - comprising a soluble parenteral
 FT formulation containing a preservative selected from an alkyl:paraben and
 FT chloro:butanol.
 PT
 XX
 PS Disclosure; Page 6; 15pp; English.
 XX

CC This sequence represents the human obesity protein. It can be used in the
 CC formulation of the invention. The formulation of the invention is a
 CC soluble parenteral formulation that comprises an obesity protein and a
 CC preservative selected from an alkyl:paraben, chlorobutanol, or a mixture.
 CC The compositions can be used for treating obesity and disorders
 CC associated with obesity. In the formulations, the obesity protein remains
 CC stable and soluble at much higher concentrations and at a pH range
 CC acceptable for a soluble, parenteral formulation
 XX
 SQ Sequence 146 AA;

Query Match 100.0%; Score 736; DB 2; Length 146;
 Best Local Similarity 100.0%; Pred. No. 9e-73;
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPIQKVDDTKTLTKITVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
 DB 1 VPIQKVDDTKTLTKITVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
 QY 61 YQQLTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
 DB 61 YQQLTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
 QY 121 TEVVALSRQGSIQDMLWQLDLSPGC 146
 DB 121 TEVVALSRQGSIQDMLWQLDLSPGC 146

RESULT 6
 AAW10151
 ID AAW10151 standard; protein; 146 AA.
 XX
 AC AAW10151;
 XX
 DT 27-AUG-2003 (revised)
 DT 02-OCT-1997 (first entry)
 XX
 DE Properly folded obesity protein intermediate.
 XX
 KW Intermediate; recombinant; production; obesity; regulation; fatty tissue;
 KW treatment; disease; diabetes; cardiovascular; cancer; properly folded.
 XX
 OS Mammalia.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /label= Val-R3
 FT /note= "R3 is absent, Met, Met-R4 or leader sequence
 FT (preferably Met-Arg, Gly-Ser-Pro or 1 of AAW08589-94),
 FT and R4 is any amino acid other than Pro"
 FT Modified-site 96

FT
 FT
 FT Modified-site 146
 FT
 FT /note= "free Cys residue or part of mixed disulfide with,
 FT e.g. Cys, glutathione or 2-mercaptoethanol when Cys146 is
 FT free Cys residue"
 FT
 FT /note= "free Cys residue or part of mixed disulfide with,
 FT e.g. Cys, glutathione or 2-mercaptoethanol when Cys96 is
 FT free Cys residue"
 XX
 PN W09700886-A1.
 XX
 XX 09-JAN-1997.
 XX
 XX 20-JUN-1996; 96WO-US010613.
 XX
 XX 22-JUN-1995; 95US-0000451P.
 XX
 XX (ELIL) LILLY & CO ELI.
 PA
 XX Hale JE, Mackellar W;
 XX WPI; 1997-087317/08.
 DR
 XX Properly folded intermediate for obesity protein - prepd. from inclusion
 XX bodies, provides high yield of active protein for treatment of obesity
 PT and its complications.
 PT
 XX
 PS Claim 1; Page 21; 66pp; English.
 XX

CC AAW10151 is a properly folded intermediate for the production of the
 CC biologically active obesity protein AAW22901, which has a similar
 CC structure but comprises a disulfide bridge between Cys96 and Cys146.
 CC AAW10151 is the final intermediate in the renaturation of a recombinant
 CC protein to AAW22901, which is an active anti-obesity protein for the
 CC regulation of fatty tissue and treatment of obesity related diseases,
 CC e.g. diabetes, cardiovascular disease and cancer. The production of
 CC AAW22901 via AAW10151 provides a high yield of active protein, and
 CC permits large scale manufacture with a high concentration of protein
 CC during the folding stage. AAW10151 already has the correct tertiary
 CC structure and conversion to AAW22901 is almost quantitative, with minimal
 CC formation of S-S linked dimers or multimers, negating the need for an
 CC aggregation preventing agent. AAW10151 is stable in the presence or
 CC absence of denaturant, is soluble in phosphate buffered saline and can be
 CC purified and characterised. (Updated on 27-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 146 AA;

Query Match 100.0%; Score 736; DB 2; Length 146;
 Best Local Similarity 100.0%; Pred. No. 9e-73;
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPIQKVDDTKTLTKITVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
 DB 1 VPIQKVDDTKTLTKITVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
 QY 61 YQQLTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
 DB 61 YQQLTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
 QY 121 TEVVALSRQGSIQDMLWQLDLSPGC 146
 DB 121 TEVVALSRQGSIQDMLWQLDLSPGC 146

RESULT 7
 AAW22901
 ID AAW22901 standard; protein; 146 AA.
 XX
 AC AAW22901;
 XX
 DT 27-AUG-2003 (revised)
 DT 02-OCT-1997 (first entry)
 XX
 DE Biologically active obesity protein.

XX Intermediate; recombinant; production; obesity; cancer; properly folded.
 KW treatment; disease; diabetes; cardiovascular; cancer; properly folded.
 KW Mammalia.
 OS
 XX Key Location/Qualifiers
 XX Modified-site 1
 FT /label= Val-R3
 FT /note= "R3 is absent, Met, Met-R4 or leader sequence
 FT (preferably Met-Arg, Gly-Ser-Pro or 1 of AAW0589-94),
 FT and R4 is any amino acid other than Pro"
 FT Disulfide-bond 96..146
 XX
 XX WO9700886-A1.
 XX
 XX 09-JAN-1997.
 XX
 XX 20-JUN-1996; 96WO-US010613.
 XX
 XX 22-JUN-1995; 95US-0000451P.
 XX
 XX (ELIL) LILLY & CO ELI.
 XX
 XX Hale JE, Mackellar W;
 XX WPI; 1997-087317/08.
 XX
 XX Properly folded intermediate for obesity protein - prepd. from inclusion
 PT bodies, provides high yield of active protein for treatment of obesity
 PT and its complications.
 XX
 XX Claim 12; Page 21; 66pp; English.

XX AAW10151 is a properly folded intermediate for the production of the
 CC biologically active obesity protein AAW22901, which has a similar
 CC structure but comprises a disulphide bridge between Cys96 and Cys146.
 CC AAW10151 is the final intermediate in the renaturation of a recombinant
 CC protein to AAW22901, which is an active anti-obesity protein for the
 CC regulation of fatty tissue and treatment of obesity related diseases,
 CC e.g. diabetes, cardiovascular disease and cancer. The production of
 CC AAW22901 via AAW10151 provides a high yield of active protein, and
 CC permits large scale manufacture with a high concentration of protein
 CC during the folding stage. AAW10151 already has the correct tertiary
 CC structure and conversion to AAW22901 is almost quantitative, with minimal
 CC formation of S-S linked dimers or multimers, negating the need for an
 CC aggregation preventing agent. AAW10151 is stable in the presence or
 CC absence of denaturant, is soluble in phosphate buffered saline and can be
 CC purified and characterised. (Updated on 27-AUG-2003 to correct OS field.)
 XX
 XX SQ Sequence 146 AA;

Query Match 100.0%; Score 736; DB 2; Length 146;
 Best Local Similarity 100.0%; Pred. No. 9e-73;
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 VPIQKVQDDTKTLIKTIIVTRINDISHTSQSVSSKOKVTGLDFIPGLHPILTLTKMDQTLAV 60
 Db 1 VPIQKVQDDTKTLIKTIIVTRINDISHTSQSVSSKOKVTGLDFIPGLHPILTLTKMDQTLAV 60
 Qy 61 YQQLTSMPSNRNVQISNDLENLRDLHLVLAFAFSKCHLPWASGLETLDSLGLGVLEASGYS 120
 Db 61 YQQLTSMPSNRNVQISNDLENLRDLHLVLAFAFSKCHLPWASGLETLDSLGLGVLEASGYS 120
 Qy 121 TEVALSRLOGLQDMLWQLDLSGPC 146
 Db 121 TEVALSRLOGLQDMLWQLDLSGPC 146

RESULT 8
 AAW30791
 ID AAW30791 standard; protein; 146 AA.
 XX

AC AAW30791;
 XX
 XX 12-MAR-1998 (first entry)
 DT
 XX Obesity protein complexed with a divalent metal cation.
 DE
 XX Obesity protein; diabetes; cancer; cardiovascular disease;
 KW divalent metal cation; leader sequence.
 KW
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FT Disulfide-bond 96..146
 XX
 XX WO9728824-A1.
 XX
 XX 14-AUG-1997.
 XX
 XX 24-JAN-1997; 97WO-US001188.
 XX
 XX 06-FEB-1996; 96US-0011238P.
 XX
 XX (ELIL) LILLY & CO ELI.
 XX
 XX Hoffmann JA;
 XX WPI; 1997-415077/38.
 XX
 XX New compound comprising obesity protein and divalent metal cation - for
 PT treatment of obesity and associated conditions, required at lower dose
 PT than free protein.
 XX
 XX Claim 3; Page 26; 33pp; English.
 XX
 XX The present sequence represents a human obesity protein, which is
 CC complexed with a divalent metal cation e.g. zinc and optionally has a
 CC leader sequence. It is used to treat obesity and conditions (particularly
 CC type II diabetes, cardiovascular disease and cancer) associated with it.
 CC When formulated with the metal ion, it is more active, allowing reduction
 CC in dose and thus reduction in cost and toxic side effects
 XX
 XX SQ Sequence 146 AA;
 Query Match 100.0%; Score 736; DB 2; Length 146;
 Best Local Similarity 100.0%; Pred. No. 9e-73;
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 VPIQKVQDDTKTLIKTIIVTRINDISHTSQSVSSKOKVTGLDFIPGLHPILTLTKMDQTLAV 60
 Db 1 VPIQKVQDDTKTLIKTIIVTRINDISHTSQSVSSKOKVTGLDFIPGLHPILTLTKMDQTLAV 60
 Qy 61 YQQLTSMPSNRNVQISNDLENLRDLHLVLAFAFSKCHLPWASGLETLDSLGLGVLEASGYS 120
 Db 61 YQQLTSMPSNRNVQISNDLENLRDLHLVLAFAFSKCHLPWASGLETLDSLGLGVLEASGYS 120
 Qy 121 TEVALSRLOGLQDMLWQLDLSGPC 146
 Db 121 TEVALSRLOGLQDMLWQLDLSGPC 146
 RESULT 9
 AAW26194
 ID AAW26194 standard; protein; 146 AA.
 XX
 XX AAW26194;
 XX
 XX 18-FEB-1998 (first entry)
 DT
 XX Obesity protein analogue #6.
 DE
 XX Obesity protein analogue; divalent metal cation complex; therapy; cancer;
 KW obesity; obesity associated disorder; diabetes; cardiovascular disease.
 KW
 XX

OS Synthetic.
XX Key Location/Qualifiers
PH Disulfide-bond 96. .146
FT Misc-difference 97
FT /note= "optionally replaced with Gln, Asn, Ala, Gly, Ser
or Pro"
FT Misc-difference 100
FT /note= "optionally replaced with Ala, Glu, Asp, Asn, Met,
Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val or Leu"
FT Misc-difference 101
FT /note= "optionally replaced with Ser, Asn, Gly, His, Pro,
Thr or Val"
FT Misc-difference 102
FT /note= "optionally replaced with Arg"
FT Misc-difference 103
FT /note= "optionally replaced with Ala"
FT Misc-difference 105
FT /note= "optionally replaced with Gln"
FT Misc-difference 106
FT /note= "optionally replaced with Lys or Ser"
FT Misc-difference 107
FT /note= "optionally replaced with Pro"
FT Misc-difference 108
FT /note= "optionally replaced with Glu"
FT Misc-difference 111
FT /note= "optionally replaced with Asp"
FT Misc-difference 138
FT /note= "optionally replaced with Ala, Glu, Asp, Asn, Met,
Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val or Leu"
FT
FT
XX WO9726916-A1.
XX
XX
XX
PD 31-JUL-1997.
XX
XX 24-JAN-1997; 97WO-US001189.
XX
XX 25-JAN-1996; 96US-0011055P.
XX
XX (ELIL) LILLY & CO ELI.
XX Hoffmann JA;
XX
XX WPI; 1997-393377/36.
XX Obesity protein analogue complexed with divalent metal cation - useful
PT for treating obesity and associated disorders, e.g. diabetes,
PT cardiovascular disease and cancer.
XX
XX Disclosure; Page 11; 45pp; English.
XX
XX AAW26189, AAW26190 and AAW26192-W26201 represent obesity protein
CC analogues contained in the compound of the invention. These sequences
CC were synthetically created from the sequence shown in AAW26191. The
CC compound of the invention comprises one of these obesity protein
CC analogues complexed with a divalent metal cation (preferably Zn⁺⁺). The
CC specification does not indicate where the divalent metal cation complexes
CC to on the obesity protein analogue. The compound of the invention (or a
CC parenteral pharmaceutical formulation containing it) can be used to treat
CC obesity. It may also be used to treat disorders associated with obesity
CC such as diabetes, cardiovascular disease and cancer. The compound allows
CC effective pharmacological treatment at lower doses that significantly
CC reduce the risk of toxic or other undesirable effects. In addition,
CC because the amount of protein administered is less, the cost of the unit
CC dosage form to the patient is reduced
XX
XX Sequence 146 AA;
Query Match 100.0%; Score 736; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 9e-73;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

Db 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
QY 61 YQOILTSMPSRNVIOISNDLENRLDLLHLVLAFSKSLPWSAGLETLDLSLGGVLEASGYS 120
Db 61 YQOILTSMPSRNVIOISNDLENRLDLLHLVLAFSKSLPWSAGLETLDLSLGGVLEASGYS 120
QY 121 TEVVALSRLQGSLODMLWQDLSPGC 146
Db 121 TEVVALSRLQGSLODMLWQDLSPGC 146
RESULT 10
AAW34483
ID AAW34483 standard; protein; 146 AA.
XX
AC AAW34483;
XX
DT 17-MAR-1998 (first entry)
XX Human obesity protein.
XX
XX Obesity protein; therapy; obesity associated disorder; human.
XX
XX Homo sapiens.
XX
XX EP784981-A2.
XX
XX 23-JUL-1997.
XX
XX 17-JAN-1997; 97EP-00300300.
XX
XX 19-JAN-1996; 96US-0010357P.
XX 07-FEB-1996; 96GB-00002410.
XX
XX (ELIL) LILLY & CO ELI.
XX
XX Beals JM, Dodd SW, Millican RL, Pekar AH;
XX
XX WPI; 1997-365737/34.
XX
XX New obesity protein compositions - comprising a soluble parenteral
PT formulation containing a preservative and having low ionic strength.
XX
XX Disclosure; Page 7; 17pp; English.
XX
XX This sequence represents the human obesity protein. It can be used in the
CC formulation of the invention. The formulation of the invention is a
CC soluble parenteral formulation that comprises an obesity protein and a
CC preservative, the formulation having an ionic strength of less than about
CC 10 mM. The compositions can be used for treating obesity and disorders
CC associated with obesity. In the formulations the obesity protein remains
CC soluble at much higher concentration and at the desired pH range
XX
XX Sequence 146 AA;
Query Match 100.0%; Score 736; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 9e-73;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Db 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
QY 61 YQOILTSMPSRNVIOISNDLENRLDLLHLVLAFSKSLPWSAGLETLDLSLGGVLEASGYS 120
Db 61 YQOILTSMPSRNVIOISNDLENRLDLLHLVLAFSKSLPWSAGLETLDLSLGGVLEASGYS 120
QY 121 TEVVALSRLQGSLODMLWQDLSPGC 146
Db 121 TEVVALSRLQGSLODMLWQDLSPGC 146

RESULT 11
AAW32575
ID AAW32575 standard; protein; 146 AA.
XX
AC AAW32575;
XX
DT 22-JAN-1998 (first entry)
XX
DE Anti obesity protein analogue.
XX
KW Anti obesity protein analogue; neuropeptide Y; radiovascular; renal;
KW cerebral; central nervous system; CNS; heart; blood vessel;
KW sympathetic nerve; mouse; human; pain; nociception;
KW abnormal gastrointestinal motility; secretion;
KW abnormal drink intake disorder; abnormal food intake disorder;
KW sexual dysfunction; reproductive disorder; obesity.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 96..146
XX
FN EP759441-A2.
XX
PD 26-FEB-1997.
XX
PF 26-JUN-1996; 96EP-00304723.
XX
PR 30-JUN-1995; 95US-0000740P.
PR 30-JUN-1995; 95US-0000752P.
PR 27-OCT-1995; 95US-0005910P.
PR 27-OCT-1995; 95US-0005911P.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Bue-Valleskey JM, Heiman ML, Stephens TW, Tinsley FC;
XX
DR WPI; 1997-147497/14.
XX
FT New use of biologically active anti-obesity protein analogues - for
PT treating conditions associated with excess neuropeptide Y, e.g.
PT cardiovascular, renal, cerebral or CNS disorders.
XX
PS Claim 8; Page 84; 89pp; English.
XX
CC The present sequence represents an anti obesity protein analogue used in
CC the treatment or prevention of a condition associated with an excess of
CC neuropeptide Y. The protein analogue is useful in the treatment or
CC prevention of disorders or diseases pertaining to the heart, blood
CC vessels or the renal system, conditions related to increased sympathetic
CC nerve activity, cerebral diseases and diseases related to the central
CC nervous system, conditions related to pain or nociception, diseases
CC related to abnormal gastrointestinal motility and secretion, abnormal
CC drink and food intake disorders, diseases related to sexual dysfunction
CC and reproductive disorders, and conditions or disorders associated with
CC obesity. The protein analogue has improved properties due to its lower
CC isoelectric points and due to specific substitutions to the human obesity
CC protein. It is more stable than both the mouse and human obesity protein,
CC and is therefore superior therapeutic agents. It is more readily
CC formulated and stored
XX
SQ Sequence 146 AA;
Query Match 100.0%; Score 736; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 9e-73;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPIQVQDDTKLTIKTIIVTRINDISHTQSVSKQKVTGLDFTGHLPHLTLTKMDQTLAV 60
DB 1 VPIQVQDDTKLTIKTIIVTRINDISHTQSVSKQKVTGLDFTGHLPHLTLTKMDQTLAV 60
QY 61 YQILTSMPSRNVIQISNDLENLRDLHLVLAFSKCHLPWASGLETLDSLGVLASGYS 120

Db 61 YQILTSMPSRNVIQISNDLENLRDLHLVLAFSKCHLPWASGLETLDSLGVLASGYS 120
QY 121 TEVVVALSRQSLQDMLWQLDLSFGC 146
Db 121 TEVVVALSRQSLQDMLWQLDLSFGC 146
RESULT 12
AAW34489
ID AAW34489 standard; protein; 146 AA.
XX
AC AAW34489;
XX
DT 17-MAR-1998 (first entry)
XX
DE Obesity protein analogue #5.
XX
KW Obesity protein analogue; obesity associated disorder; therapy.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 97 /note= "optionally replaced with Gln, Asn, Ala, Gly, Ser,
FT or Pro"
FT Misc-difference 100
FT /note= "optionally replaced with Arg"
FT Misc-difference 101 /note= "optionally replaced with Glu, Ala, Asp, Asn, Met,
FT Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val, or Leu"
FT Misc-difference 102 /note= "optionally replaced with Ser, Asn, Gly, His, Pro,
FT Thr, or Val"
FT Misc-difference 103 /note= "optionally replaced with Ala"
FT Misc-difference 105 /note= "optionally replaced with Gln"
FT Misc-difference 106 /note= "optionally replaced with Lys or Ser"
FT Misc-difference 107 /note= "optionally replaced with Pro"
FT Misc-difference 108 /note= "optionally replaced with Glu"
FT Misc-difference 111 /note= "optionally replaced with Asp"
FT Misc-difference 138 /note= "optionally replaced with Ala, Glu, Asp, Asn, Met,
FT Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val, or Leu"
XX
PN EP784982-A2.
XX
PD 23-JUL-1997.
XX
PF 17-JAN-1997; 97EP-00300302.
XX
PR 19-JAN-1996; 96US-0010257P.
PR 07-FEB-1996; 96GB-00002409.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Beals JM, Dodd SW, Pekar AH;
XX
DR WPI, 1997-365738/34.
XX
FT New obesity protein analogue compositions - comprising a soluble
PT parenteral formulation containing a preservative selected from an
PT alkylparaben and chlorobutanol.
XX
PS Disclosure; Page 10; 46pp; English.
XX
CC This sequence represents an obesity protein analogue, and can be used in
CC the formulation of the invention. The formulation of the invention is a

soluble parenteral formulation that comprises an obesity protein analogue and a preservative selected from an alkylparaben, chlorobutanol, or a mixture. The compositions can be used for the treatment of obesity and disorders associated with obesity. In the formulations, the obesity protein analogue remains stable and soluble at much higher concentrations and at a pH range acceptable for a soluble, multi-use parenteral formulation

Query Match 100.0%; Score 736; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 9e-73;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPIQKVDDTKTIKTVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 1 VPIQKVDDTKTIKTVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
QY 61 YQOILTSMPSRNVQISNDLENLRLDLHLVLAFAKSKCHLPWASGLETLDSLGGLVLEASGYS 120
DB 61 YQOILTSMPSRNVQISNDLENLRLDLHLVLAFAKSKCHLPWASGLETLDSLGGLVLEASGYS 120
QY 121 TEVVALLRQGSLODMWQDLSPGC 146
DB 121 TEVVALLRQGSLODMWQDLSPGC 146

RESULT 13
AAW69682
ID AAW69682 standard; protein; 146 AA.

XX AAW69682;

DT 07-DEC-1998 (first entry)

DE Human obesity protein.

XX Obesity protein; therapy; human.

XX Homo sapiens.

XX WO9831391-A1.

XX 23-JUL-1998.

XX 16-JAN-1998; 98WO-US000939.

XX 17-JAN-1997; 97US-0035714P.

XX 07-AUG-1997; 97US-0054886P.

XX (ELIL) LILLY & CO ELI.

XX Rinella JV;

XX WPI; 1998-413818/35.

PT Obesity protein soluble formulation for treating obesity - has pH greater than 8.0, at which aggregation of obesity proteins by preservatives is reduced allowing production of multi-use formulation.

PS Disclosure; Page 11-12; 30pp; English.

XX This is the amino acid sequence of human obesity protein. The invention discloses a storage-stable, soluble formulation comprising an obesity protein and a preservative, and having a pH greater than 8.0. The obesity protein used in the formulation is preferably bio-synthesised in a host cell transformed with a recombinant DNA comprising a synthetic or semi-synthetic DNA encoding the protein. The soluble formulation can be administered to mammals to treat obesity (claimed), especially humans when the obesity protein is human obesity protein. It was found that the physical stability of obesity proteins in the presence of preservatives such as phenol and cresol changes abruptly and is greatly enhanced at pH values above 8.0, such that the aggregation of obesity proteins caused by

CC preservatives is reduced. At pH above 8.0, obesity proteins remain in solution in the presence of certain preservatives, making possible a multi-use parenteral formulation containing those preservatives

XX SQ Sequence 146 AA;

Query Match 100.0%; Score 736; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 9e-73;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTIKTVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 1 VPIQKVDDTKTIKTVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

QY 61 YQOILTSMPSRNVQISNDLENLRLDLHLVLAFAKSKCHLPWASGLETLDSLGGLVLEASGYS 120

DB 61 YQOILTSMPSRNVQISNDLENLRLDLHLVLAFAKSKCHLPWASGLETLDSLGGLVLEASGYS 120

QY 121 TEVVALLRQGSLODMWQDLSPGC 146

DB 121 TEVVALLRQGSLODMWQDLSPGC 146

RESULT 14
AAW53342
ID AAW53342 standard; protein; 146 AA.

XX AAW53342;

XX 20-JUL-1998 (first entry)

XX Obesity protein analogue formula II SEQ ID NO:4.

XX Human; obesity protein; soluble; parenteral formulation; anionic;

KW amphiphilic; ob gene; Ob protein.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 97 /note= "His can be replaced with Gln, Asn, Ala, Gly, Ser, or Pro"

FT Misc-difference 100 /note= "Trp can be replaced with Ala, Glu, Asp, Asn, Met, Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val, or Leu"

FT Misc-difference 101 /note= "Ala can be replaced with Ser, Asn, Gly, His, Pro, Thr, Val"

FT Misc-difference 102 /note= "Ser can be replaced with Arg"

FT Misc-difference 103 /note= "Gly can be replaced with Ala"

FT Misc-difference 105 /note= "Glu can be replaced with Gln"

FT Misc-difference 106 /note= "Thr can be replaced with Lys or Ser"

FT Misc-difference 107 /note= "Leu can be replaced with Pro"

FT Misc-difference 108 /note= "Asp can be replaced with Glu"

FT Misc-difference 111 /note= "Gly can be replaced with Asp"

FT Misc-difference 138 /note= "Trp can be replaced with Ala, Glu, Asp, Asn, Met, Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val, or Leu; or a pharmaceutically acceptable salt thereof"

PN EP827750-A2.

XX 11-MAR-1998.

XX 22-AUG-1997; 97EP-00306420.

XX

PR 23-AUG-1996; 96US-0024121P.
 PR 23-AUG-1996; 96US-0025207P.
 XX
 PA (ELIL) LILLY & CO ELI.
 XX
 PI Beals JM, Rinella JV;
 XX
 DR WPI; 1998-180894/17.
 XX
 PT Parenteral obesity protein formulations - containing anionic amphiphilic
 PT solubiliser and stabiliser.
 XX
 PS Disclosure; Page 9; 45pp; English.
 XX
 CC The present sequence represents an obesity protein generic formula for
 CC producing obesity protein analogues for use in the present invention as
 CC part of a soluble parenteral formulation. The soluble parenteral
 CC formulations comprises an obesity protein or obesity protein analogue and
 CC an anionic amphiphilic compound. The formulations are used for treating
 CC obesity and associated disorders. The proteins are preferably present at
 CC a concentration of 5-50 mg/ml. The anionic amphiphilic compound
 CC solubilises and stabilises the protein
 XX
 SQ Sequence 146 AA;

Query Match 100.0%; Score 736; DB 2; Length 146;
 Best Local Similarity 100.0%; Pred. No. 9e-73;
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
 Db 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

Qy 61 YQQLTSMPSNRNVQISNDLENRLDLHLVLAFSKSLPWASGLETLDSLGGVLEASGYS 120
 Db 61 YQQLTSMPSNRNVQISNDLENRLDLHLVLAFSKSLPWASGLETLDSLGGVLEASGYS 120

Qy 121 TEVVALSRLOQSLQDMLWQLDLSPGC 146
 Db 121 TEVVALSRLOQSLQDMLWQLDLSPGC 146

RESULT 15

AA43311
 ID AA43311 standard; protein; 146 AA.
 XX
 AC AA43311;
 XX
 DT 21-JAN-2000 (first entry)
 XX
 DE Human leptin.
 XX
 KW Leptin; brain function improver; brain denaturation disease; therapy;
 KW Alzheimer's disease; old age dementia; Pick's disease;
 KW hereditary aphasia; Huntington's chorea; Parkinson's disease;
 KW progressive subcutaneous gliosis; progressive supranuclear paralysis;
 KW thalamus denaturation; myoclonus epilepsy.
 XX
 OS Homo sapiens.
 XX
 PN JP11279074-A.
 XX
 PD 12-OCT-1999.
 XX
 PF 26-MAR-1998; 98JP-00100202.
 XX
 PR 26-MAR-1998; 98JP-00100202.
 XX
 PA (OMUR/) OMURA H.
 PA (HORI/) HORI N.
 -PA (SHIR/) SHIRAISHI T.
 PA (SASA/) SASAKI K.
 PA (TAKE/) TAKEDA H.

PA (TSUJ/) TSUJI M.
 PA (MATS/) MATSUMIYA T.
 XX
 DR WPI; 1999-629222/54.
 XX
 PT A brain function improver - useful for treating brain disorientation
 PT diseases.
 XX
 PS Disclosure; Page 5; 11pp; Japanese.
 XX
 CC This sequence represents human leptin. The invention relates to a brain
 CC function improver containing mammalian leptin as the active component.
 CC The brain function improver is useful as a treating agent for brain
 CC denaturation diseases such as Alzheimer's disease, old age dementia,
 CC Pick's disease, Huntington's chorea, Parkinson's disease, Parkinson
 CC syndrome, progressive subcutaneous gliosis, progressive supranuclear
 CC paralysis, thalamus denaturation, hereditary aphasia and myoclonus
 CC epilepsy, and other diseases causing deterioration of brain function
 XX
 SQ Sequence 146 AA;

Query Match 100.0%; Score 736; DB 2; Length 146;
 Best Local Similarity 100.0%; Pred. No. 9e-73;
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
 Db 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

Qy 61 YQQLTSMPSNRNVQISNDLENRLDLHLVLAFSKSLPWASGLETLDSLGGVLEASGYS 120
 Db 61 YQQLTSMPSNRNVQISNDLENRLDLHLVLAFSKSLPWASGLETLDSLGGVLEASGYS 120

Qy 121 TEVVALSRLOQSLQDMLWQLDLSPGC 146
 Db 121 TEVVALSRLOQSLQDMLWQLDLSPGC 146

Search completed: May 4, 2006, 21:52:18
 Job time : 140.474 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 21:50:51 ; Search time 27.5945 seconds
(without alignments)
509.074 Million cell updates/sec

Title: US-10-623-189-1

Perfect score: 736

Sequence: 1 VPIQKVQDDTKTLIKTIVTR.....SRLGSLQDMLWQLDLSPGC 146

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_80:*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	736	100.0	167	1 LTHU	leptin precursor -
2	720.5	97.9	166	2 I33166	leptin precursor -
3	619	84.1	167	1 LTMS	leptin precursor -
4	605	82.2	167	1 LTRT	leptin precursor -
5	605	82.2	167	2 I55622	rat ob - rat
6	81.5	11.1	1600	2 A83281	glutamate dehydrog
7	80.5	10.9	444	2 S34039	hypothetical prote
8	79	10.7	829	2 T01362	probable myosin he
9	79	10.7	952	2 H84583	hypothetical prote
10	78	10.6	420	2 S75514	sensory transducti
11	78	10.6	639	2 A10055	probable soluble l
12	77.5	10.5	574	1 B42374	phosphotransferase
13	76.5	10.4	173	2 S77486	ribosomal protein
14	76.5	10.4	362	2 A83967	carbamoyl-phosphat
15	76.5	10.4	822	2 E86305	probable trehalose
16	76	10.3	409	2 B89954	hypothetical prote
17	76	10.3	570	2 T46011	hypothetical prote
18	76	10.3	1036	2 D70117	acri flavine resist
19	75.5	10.3	403	2 T26551	hypothetical prote
20	75.5	10.3	1438	2 S59792	probable membrane
21	75	10.2	142	2 C72430	hypothetical prote
22	75	10.2	296	2 D70424	5,10-methylenetet
23	75	10.2	424	2 E81358	glutamate-1-semial
24	75	10.2	1191	2 S76414	beta transducin-li
25	74.5	10.1	559	2 AB2202	hypothetical prote
26	74.5	10.1	674	2 S46092	probable membrane
27	74	10.1	177	2 A28106	prolactin, 20K - M
28	74	10.1	200	2 B32477	prolactin II precu
29	74	10.1	421	2 AB2959	exopolysaccharide

ALIGNMENTS

RESULT 1

LTHU

leptin precursor - human

N;Alternate names: obese protein; obesity factor

C;Species: Homo sapiens (man)

C;Date: 28-Jul-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004

C;Accession: A38952; JE0148

R;Zhang, Y.; Proenca, R.; Maffei, M.; Barone, M.; Leopold, L.; Friedman, J.M.

Nature 372, 425-432, 1994

A;Title: Positional cloning of the mouse obese gene and its human homologue.

A;Reference number: S50863; MUID:95075453; PMID:7984236

A;Accession: A38952

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-167 <ZHA>

A;Cross-references: UNIPROT:P41159; UNIPARC:UPI000000308D4; GB:U18915; NID:96233331; PID:

R;Liao, H.J.; Deng, Y.B.; Chen, X.M.; Ye, Y.Z.

Chinese Biochem. J. 13, 249-253, 1997

A;Title: Cloning of chinese obesity gene and construction of prokaryotic expression ve

A;Reference number: JE0148

A;Accession: JE0148

A;Molecule type: mRNA

A;Residues: 'M', 22-167 <LJA>

A;Cross-references: UNIPARC:UPI0000158347

A;Experimental source: adipose

A;Note: the author translated GAC for residue 148 as Ser

C;Genetics:

A;Gene: GDB:LEP; OB; OBS

A;Cross-references: GDB:I36420; OMIM:164160

A;Map position: 7q31.3-7q31.3

C;Superfamily: leptin

C;Keywords: adipose tissue

F;1-21/Domain: signal sequence #status predicted <SIG>

F;22-167/Product: leptin #status predicted <MAT>

Query Match 100.0%; Score 736; DB 1; Length 167;

Best Local Similarity 100.0%; Pred. No. 1.6e-59;

Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60
DB 22 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 81

QY 61 YQOILTSPNSRNVIQISNDLENRLDLHLVLAFLPSKCHLPWASGLTFLDSLGVLBASGV 120
DB 82 YQOILTSPNSRNVIQISNDLENRLDLHLVLAFLPSKCHLPWASGLTFLDSLGVLBASGV 141

QY 121 TEVALSRLQSLQDMLWQLDLSPGC 146

DB 142 TEVALSRLQSLQDMLWQLDLSPGC 167

exopolysaccharide
alkaline phosphata
kinesin family pro
probable methyl-ac
hypothetical prote
conserved hypochet
ATP-dependent RNA
type III secretion
hypothetical prote
phenylalanine-TRNA
probable yopC/gen
probable membrane
hypothetical prote
keratin 20, type I
14-nm filament pro
hypothetical prote

RESULT 12

B42374
phosphotransferase system enzyme I (EC 2.7.3.9) - *Staphylococcus carnosus*
C:Species: *Staphylococcus carnosus*
C>Date: 10-Jul-1992 #sequence_revision 31-Jan-1997 #text_change 09-Jul-2004
C:Accession: B42374; S17075
R:Kohlbrecher, D.; Eisermann, R.; Hengstenberg, W.
J. Bacteriol. 174, 2208-2214, 1992
A:Title: *Staphylococcal* phosphoenolpyruvate-dependent phosphotransferase system: molecular studies of the gene product.
A:Reference number: A42374; MUID:92202148; PMID:1551842
A:Accession: B42374
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-574 <KOH>
A:Cross-references: UNIPROT:P23533; UNIPARC:UPI000013287C; GB:M69050; NID:gl53073; PIDN:R:Eisermann, R.; Fischer, R.; Kessler, U.; Neubauer, A.; Hengstenberg, W.
Eur. J. Biochem. 197, 9-14, 1991
A:Title: *Staphylococcal* phosphoenolpyruvate-dependent phosphotransferase system. Purification and cloning of the *ptsH* gene.
A:Reference number: S15367; MUID:91200066; PMID:1901791
A:Accession: S17075
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-90 <EIS>
A:Cross-references: UNIPARC:UPI000017007F; EMBL:X60766; NID:g46907; PIDN:CAA43176.1; PIDC:Superfamily: phosphotransferase system enzyme I; phosphotransferase system enzyme I homologous domain: phosphotransferase system enzyme I homology <PT1>

F:5-563/Domain: phosphotransferase system enzyme I homology <PT1>

Query Match 10.5%; Score 77.5; DB 1; Length 574;
Best Local Similarity 25.0%; Pred. No. 34;
Matches 32; Conservative 27; Mismatches 54; Indels 15; Gaps 5;
Qy 11 KTLIKTIVTR---INDISHTQSVSSKQKVTGLDFIPGLHPLTLTKSKMDQTLAVVQOILTS 67
Db 188 RTSIAIMSRSLEIPAVVGTGKSTEEVEAGDTIVVDGVTGDLINPDSDEIVAEYQE--- 243
Qy 68 MPSRNVQISNDLENLRLHLVAFSKSCHLPWASGLETSLDGLVLE--ASG---YSTE 122
Db 244 -KRENFKDKOELQKLRDAESVTA--DGHVVELAANIQTNDLPFVIENGAEGLYRTE 300
Qy 123 VVALSRQ 130
Db 301 FLYMGDRQ 308

RESULT 13

S77486
ribosomal protein S5 - *Synechocystis* sp. (strain PCC 6803)
N:Alternate names: protein sll1812
C:Species: *Synechocystis* sp.
A:Variety: PCC 6803
C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S77486
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S77486
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-173 <KAN>
A:Cross-references: UNIPROT:P73304; UNIPARC:UPI000013507A; EMBL:D90905; GB:AB001339; NID:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Genetics:
A:Gene: rps5
C:Superfamily: ribosomal protein S5/S2
C:Keywords: protein biosynthesis; ribosome

Query Match 10.4%; Score 76.5; DB 2; Length 173;
Best Local Similarity 31.2%; Pred. No. 9.2;
Matches 29; Conservative 12; Mismatches 41; Indels 11; Gaps 3;
Qy 6 VQDPTKTIKTIIVTRINDISH-TQSVSSKQKVTGLDFIPG-----LHPILTLSKMDQ 56
Db 70 VADKKQLIEVPLTKSIIHTINGVSGAKVVRPAAPGTGVTAGAVRTVLELAGVKN 129
Qy 57 TLAVYQOILTSPSRNVQISNDLENLRLHLV 89
Db 130 ILA--KQLGSNNPLNARAAINALETLTPTSEV 160

RESULT 14

A83967
carbamoyl-phosphate synthetase (glutaminase subunit) pyzAA [imported] - *Bacillus halodurans*
C:Species: *Bacillus halodurans*
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: A83967
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujita, P.; Hir Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and sequencing of the *ptsH* gene.
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: A83967
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-362 <STO>
A:Cross-references: UNIPROT:Q9K9V8; UNIPARC:UPI0000126F32; GB:AP001515; GB:BA000004; NID:Experimental source: strain C-125
C:Genetics:
A:Gene: pyzAA
C:Superfamily: carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain; carbam

Query Match 10.4%; Score 76.5; DB 2; Length 362;
Best Local Similarity 31.0%; Pred. No. 23;
Matches 22; Conservative 15; Mismatches 27; Indels 7; Gaps 3;
Qy 78 NDLENRLDLHLVAFSKSCHLP--WASGLETSLDGLVLEASGYG---TEVVALSRQ 131
Db 66 DDPESMPAIGHGLIVKEACDIPSNRSE-ESLDSLKAKQIPGLSGIDTRKLRIRMHG 124
Qy 132 SLQDMLWQLDL 142
Db 125 TLKQLCPLDV 135

RESULT 15

E86305
probable trehalose-6-phosphate synthase [imported] - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: E86305
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, M.A.; Kaul, S.; White, O.; Alonso, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. Chin. C.W.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E86305
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-822 <STO>
A:Cross-references: UNIPROT:Q9FZ57; UNIPARC:UPI00000A0CF7; GB:AE005172; NID:g9802765; C:Genetics:
A:Map position: 1

Query Match 10.4%; Score 76.5; DB 2; Length 822;
Best Local Similarity 31.6%; Pred. No. 66;

Matches 31; Conservative 16; Mismatches 36; Indels 15; Gaps 4;
-Qy 38 GLDFIPGLHPILTLSKMDQTLAVYQQILTSMPSRNVIQISNDLENLRDLLHVLAFKSCH 97
Db 470 GLDFMSELNGIIPESQM-----RKIPLOLPEQDVIQQYSQNN---RLIILGFFGTLA 521
Qy 98 LPWASGLETLD-----SLGGVLEA--SGYSTEVVALSR 128
Db 522 EPMNSGTKEMDLKLNPELKGTLKALCNDPKTIVVVLRS 559

Search completed: May 4, 2006, 22:03:30
Job time : 28.5945 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 21:47:48 ; Search time 145.498 Seconds
(without alignments)
707.961 Million cell updates/sec

Title: US-10-623-189-1
Perfect score: 736
Sequence: 1 VPIQVQDDPKTKTIKTIIVTR.....SRLQGSILQMLQDLSPGC 146

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	736	100.0	167	1	OB_HUMAN	P41159 homo sapien
2	736	100.0	167	1	O6NT58_HUMAN	O6NT58 homo sapien
3	733	99.6	146	1	OB_PANTR	O02750 pan troglod
4	728	98.9	146	1	OB_GORGO	Q95189 gorilla gor
5	721	98.0	146	1	OB_PONPY	Q95234 pongo pygma
6	672	91.3	167	1	OB_MACMU	Q28504 macaca mula
7	639	86.8	167	1	OB_FELCA	Q9n2c1 felis silve
8	628	85.3	146	2	O6T8R8_BUBBU	O6T8R8 bubalus bub
9	628	85.3	167	1	OB_BOVIN	P50595 bos taurus
10	628	85.3	167	1	OB_BUBBU	Q5J732 bubalus bub
11	627	85.2	167	1	OB_PIG	Q29406 sus scrofa
12	627	85.2	167	2	O5TIL9_PIG	Q5TIL9 sus scrofa
13	624	84.8	146	1	OB_SHEEP	Q28603 ovis aries
14	624	84.8	167	1	O5E8A4_BOVIN	O5E8A4 bos taurus
15	619	84.1	146	2	Q4VW71_CTEID	Q4VW71 ctenopharyn
16	619	84.1	167	1	OB_MOUSE	P41160 mus musculus
17	619	84.1	167	2	Q544U0_MOUSE	Q544U0 mus musculus
18	615	83.6	146	2	Q4VW70_HYPMO	Q4VW70 hypophthalm
19	615	83.6	146	2	Q4VW72_CARAU	Q4VW72 carassius a
20	615	83.6	146	2	Q4ILM8_CYPECA	Q4ILM8 cyprinus ca
21	612	83.2	146	2	Q4VW67_MEGAM	Q4VW67 megalobrama
22	609	82.7	146	2	Q4VW68_SILAS	Q4VW68 silurus aso
23	605	82.2	167	1	OB_RAT	P50596 rattus norv
24	604	82.1	146	2	Q4VW66_9PERC	Q4VW66 channa argu
25	604	82.1	146	2	Q4VW81_9TELE	Q4VW81 culter sp.
26	603.5	82.0	147	2	Q4VW60_ANAPL	Q4VW60 anas platyr
27	597	81.1	146	2	Q4VW69_ARINO	Q4VW69 aristichy
28	596	81.0	167	1	OB_CANFA	O02720 canis famil
29	586.5	79.7	163	1	OB_CHICK	O42164 gallus gall
30	576.5	78.3	145	1	OB_MELGA	O93416 meleagris g
31	522.5	71.0	145	1	OB_HORSE	O9TU09 equus cabal

32 505 68.6 167 1 OB_SMICK
33 499 67.8 118 2 Q4VYB6_9RODE
34 498 67.7 119 2 Q861R2_BUBBU
35 477 64.8 118 2 Q8MK60_ALOLA
36 476 64.7 118 2 Q8MK58_VULVU
37 474 64.4 118 2 Q8MK59_NYCPK
38 469 63.7 118 2 Q8MK61_CANFA
39 465 63.2 167 1 OB_HALGR
40 463 62.9 167 1 OB_PHOVI
41 462 62.8 123 2 Q95KW9_MYOIU
42 457 62.1 110 2 Q56Q08_SHEEP
43 449 61.0 109 2 Q866S7_BUBBU
44 439 59.6 109 2 Q864V1_CAMDR
45 387 52.6 106 2 Q95WGS_CAPHI

ALIGNMENTS

RESULT 1
OB_HUMAN STANDARD; PRT; 167 AA.
AC P41159; O15158; Q56A88;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Leptin precursor (Obesity factor) (Obese protein).
GN Name=LEP; Synonyms=OB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95075453; Pubmed=7984236; DOI=10.1038/372425a0;
RA Zhang Y., Proenca P., Maffei M., Barone M., Leopold L., Friedman J.M.;
RT "Positional cloning of the mouse obese gene and its human homologue.";
RL Nature 372:425-432(1994).
RN [2]
RP ERATUM.
RA Zhang Y., Proenca P., Maffei M., Barone M., Leopold L., Friedman J.M.;
RL Nature 374:479-479(1995).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95309556; Pubmed=7789654;
RA Masuzaki H., Ogawa Y., Isse N., Satoh N., Okazaki T., Shigemoto M.,
Mori K., Tamura N., Hosoda K., Yoshimasa Y., Jingami H., Kawada T.,
Nakao K.;
RT "Human obese gene expression. Adipocyte-specific expression and
regional differences in the adipose tissue.";
RL Diabetes 44:855-858(1995).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96223959; Pubmed=8626726; DOI=10.1074/jbc.271.8.3971;
RA Gong D.W., Bi S., Pratley R.E., Weintraub B.D.;
RT "Genomic structure and promoter analysis of the human obese gene.";
RL J. Biol. Chem. 271:3971-3974(1996).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX Chehab F.P., Lim M.B.;
RA Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96070903; Pubmed=7499240; DOI=10.1074/jbc.270.46.27728;
RA Isse N., Ogawa Y., Tamura N., Masuzaki H., Mori K., Okazaki T.,
Satoh N., Shigemoto M., Yoshimasa Y., Nishi S., Hosada K., Inazawa J.,
Nakao K.;
RT "Structural organization and chromosomal assignment of the human obese
gene.";
RL J. Biol. Chem. 270:27728-27733(1995).
RN [7]
RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=96198511; PubMed=8621021;
 RA Niki T., Mori H., Tamori Y., Kishimoto-Hashiramoto M., Ueno H.,
 RA Akaki S., Masugi J., Sawant N., Majithia H.R., Rais N.,
 RA Hashiramoto M., Taniguchi H., Kasuga M.;
 RT "Human obese gene: molecular screening in Japanese and Asian Indian
 RT NIDDM patients associated with obesity.";
 RL Diabetes 45:675-678(1996).
 [8]
 RN NUCLEOTIDE SEQUENCE [MRNA].
 RA Lu L., Fu Z., Xu M., Fu Y., Hu Z.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 [9]
 RN NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANT MET-94.
 RA Rieder M.J., Johanson E.J., da Ponte S.H., Hastings N.C., Ahearn M.O.,
 RA Bartucci C.B., Wong M.W., Yi Q., Nickerson D.A.;
 RT "SeattleSNPs: NHLBI H66682 program for genomic applications, UW-
 RT FCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 [10]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Placenta; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.C., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [11]
 RN INTERACTION WITH SIGLEC6.
 RX MEDLINE=99357812; PubMed=10428856; DOI=10.1074/jbc.274.32.22729;
 RA Patel N., Brinkman-Van der Linden E.C.M., Altmann S.W., Gish K.C.,
 RA Balasubramanian S., Timans J.C., Peterson D., Bell M.P., Bazan J.F.,
 RA Varki A., Kastelein R.A.;
 RT "OB-BP1/Siglec-6. A leptin- and sialic acid-binding protein of the
 RT immunoglobulin superfamily.";
 RL J. Biol. Chem. 274:22729-22738(1999).
 [12]
 RN ERRATUM.
 RA Patel N., Brinkman-Van der Linden E.C.M., Altmann S.W., Gish K.C.,
 RA Balasubramanian S., Timans J.C., Peterson D., Bell M.P., Bazan J.F.,
 RA Varki A., Kastelein R.A.;
 RL J. Biol. Chem. 274:28058-28058(1999).
 [13]
 RN STRUCTURE BY NMR.
 RX MEDLINE=97309492; PubMed=9166907; DOI=10.1016/S0014-5793(97)00353-0;
 RA Kline A.D., Becker G.W., Churgay L.M., Landen B.E., Martin D.K.,
 RA Muth W.L., Rathnachalam R., Richardson J.M., Schoner B., Ulmer M.,
 RA Hale J.E.;
 RT "Leptin is a four-helix bundle: secondary structure by NMR.";
 RL FEBS Lett. 407:239-242(1997).
 [14]
 RN X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
 RX MEDLINE=97289390; PubMed=9144295;
 RA Zhang F., Basinski M.B., Beals J.M., Briggs S.L., Churgay L.M.,
 RA Clawson D.K., Dimarchi R.D., Furman T.C., Hale J.E., Hsiung H.M.,
 RA Schoner B.E., Smith D.P., Zhang X.Y., Wery J.P., Schevitz R.W.;
 RT "Crystal structure of the obese protein leptin-E100.";
 RL Nature 387:206-209(1997).

RN VARIANT MET-94.
 RA Bartholomew D.W., McClellan J.M.;
 RT "A novel polymorphism in the leptin gene.";
 RL Hum. Mutat. 12:220-220(1998).
 [16]
 RN VARIANT MORBID OBESITY TRP-105.
 RX MEDLINE=98160176; PubMed=9500540;
 RA Strobel A., Issad T., Camoin L., Ozata M., Strosberg A.D.;
 RT "A leptin missense mutation associated with hypogonadism and morbid
 RT obesity.";
 RL Nat. Genet. 18:213-215(1998).
 CC -1- FUNCTION: May function as part of a signaling pathway that acts to
 CC regulate the size of the body fat depot. An increase in the level
 CC of LEP may act directly or indirectly on the CNS to inhibit food
 CC intake and/or regulate energy expenditure as part of a homeostatic
 CC mechanism to maintain constancy of the adipose mass.
 CC -1- SUBUNIT: Interacts with SIGLEC6.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DISEASE: Defects in LEP may be a cause of autosomal recessive
 CC obesity [MIM:601665].
 CC -1- SIMILARITY: Belongs to the leptin family.
 CC -1- DATABASE: NAME=R&D Systems' cytokine mini-reviews: LEP;
 CC WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyid=213".

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 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

 DR EMBL; U18915; AAA60470.1; -; mRNA.
 DR EMBL; D49487; BAA08448.1; -; mRNA.
 DR EMBL; U43653; AAC50400.1; -; mRNA.
 DR EMBL; U43415; AAC31660.1; -; Genomic DNA.
 DR EMBL; D63710; BAA09839.1; -; Genomic DNA.
 DR EMBL; D63519; BAA09787.1; -; Genomic DNA.
 DR EMBL; AF008123; AAB63507.1; -; mRNA.
 DR EMBL; AY986373; AAX81413.1; -; Genomic DNA.
 DR EMBL; BC060830; AAB60830.1; -; mRNA.
 DR EMBL; BC069452; AAB69452.1; -; mRNA.
 DR EMBL; BC069527; AAB69527.1; -; mRNA.
 DR PIR; A38952; LTHU.
 DR PIR; I53166; I53166.
 DR PDB; 1AX8; X-ray; @=22-167.
 DR Ensembl; ENSG00000174697; Homo sapiens.
 DR HGNC; HGNC:6553; LEP.
 DR MIM; 164160; -.
 DR MIM; 601665; -.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0006112; P:energy reserve metabolism; TAS.
 DR InterPro; IPR012351; Cytokine_4_hlx.
 DR InterPro; IPR000065; Leptin.
 DR PANTHER; PTHR11724; Leptin; 1.
 DR Pfam; PF02024; Leptin; 1.
 DR PRINTS; PR00495; LEPTIN.
 DR ProDom; PD005698; Leptin; 1.
 DR 3D-structure; Diabetes mellitus; Disease mutation; Obesity;
 KW Polymorphism; Signal.
 FT SIGNAL 1 21 Potential.
 FT CHAIN 22 167 Leptin.
 FT DISULFID 117 167
 FT VARIANT 49 49 Missing (in 30% the clones).
 FT VARIAT 94 94 /FTID=VAR_004196.
 FT VARIAT 105 105 V -> M (in dbSNP:17151919).
 FT VARIAT 110 110 R -> W (in morbid obesity and
 FT VARIAT 110 110 hypogonadism).
 FT VARIAT 96 96 /FTID=VAR_008094.
 FT CONFLICT 96 96 V -> M (in dbSNP:1800564).
 FT HELIX 25 44 Q -> R (in Ref. 8).

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FT HELIX 72 87
FT TURN 88 88

Query Match 100.0%; Score 736; DB 1; Length 167;
Best Local Similarity 100.0%; Pred. No. 9.1e-60; Indels 0; Gaps 0;
Matches 146; Conservative 0; Mismatches 0;

QY 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIFGLHPILTLTKMDQTLAV 60
DB 22 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIFGLHPILTLTKMDQTLAV 81

QY 61 YQILTSMPSRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
DB 82 YQILTSMPSRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYS 141

QY 121 TEVVALSRLOGLQDMLWQDLSPGC 146
DB 142 TEVVALSRLOGLQDMLWQDLSPGC 167

RESULT 2
Q6NT58_HUMAN
ID Q6NT58_HUMAN PRELIMINARY; PRT; 167 AA.
AC Q6NT58;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Leptin.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.B., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Rana S.S., Loquellano N.A., Peters G.J., Casavant T.L., Prange C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RA Strausberg R.;
RA Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: May function as part of a signaling pathway that acts to
CC regulate the size of the body fat depot. An increase in the level
CC of LEP may act directly or indirectly on the CNS to inhibit food
CC intake and/or regulate energy expenditure as part of a homeostatic
CC mechanism to maintain constancy of the adipose mass (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC EMBL; BC069323; AA069323.1; -; mRNA.
CC HSSP; P41159; IAX8.
CC SMR; Q6NT58; 24-167.
CC
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DR Ensembl; ENSG00000174697; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR012351; Cytokine_4_hlx.
DR InterPro; IPR000085; Leptin.
DR Pfam; PF02024; Leptin; 1.
DR PRINTS; PR00495; LEPTIN.
DR ProDom; PD005698; Leptin; 1.
SQ SEQUENCE 167 AA; 18613 MW; BE1A046PFB1554DE CRC64;

Query Match 100.0%; Score 736; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 9.1e-60; Indels 0; Gaps 0;
Matches 146; Conservative 0; Mismatches 0;

QY 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIFGLHPILTLTKMDQTLAV 60
DB 22 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIFGLHPILTLTKMDQTLAV 81

QY 61 YQILTSMPSRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
DB 82 YQILTSMPSRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYS 141

QY 121 TEVVALSRLOGLQDMLWQDLSPGC 146
DB 142 TEVVALSRLOGLQDMLWQDLSPGC 167

RESULT 3
OB_PANTR
ID OB_PANTR STANDARD; PRT; 146 AA.
AC O02750;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Leptin (Obesity factor).
GN Names=LEP; Synonyms=OB;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pan.
OX NCBI_TaxID=9598;
RN [1]
NUCLEOTIDE SEQUENCE.
RC Schoner B., Basinski M.B., Smith D.P., Hsiung H.M., Zhang X.,
RC Rockey P.K., Rostock P.R.;
RA "Cloning of obese genes from different species: a comparison of the
RA gene structures and the sequences of the obese gene products,
RA leptin."
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: May function as part of a signaling pathway that acts to
CC regulate the size of the body fat depot. An increase in the level
CC of LEP may act directly or indirectly on the CNS to inhibit food
CC intake and/or regulate energy expenditure as part of a homeostatic
CC mechanism to maintain constancy of the adipose mass (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- SIMILARITY: Belongs to the leptin family.
CC
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CC with the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; U96450; AA054023.1; -; mRNA.
CC HSSP; P41159; IAX8.
CC SMR; O02750; 3-146.
CC InterPro; IPR012351; Cytokine_4_hlx.
CC InterPro; IPR000065; Leptin.
CC PANTHER; PTHR11724; Leptin; 1.
CC Pfam; PF02024; Leptin; 1.
CC PRINTS; PR00495; LEPTIN.
CC
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DR ProDom; PD005698; Leptin; 1.
KW Obesity.
FT DISULFID 96 146 By similarity.
-SQ SEQUENCE 146 AA; 16059 MW; 02C42A06B54D55C CRC64;

Query Match 99.6%; Score 733; DB 1; Length 146;
Best Local Similarity 99.3%; Pred. No. 1.5e-59;
Matches 145; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVQDDTKLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 1 VPIQKVQDDTKLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

QY 61 YQOILTSMPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
DB 61 YQOILTSMPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYS 120

QY 121 TEVVALSRQGSIQDMLWQLDLSPGC 146
DB 121 TEVVALSRQGSIQDMLWQLDLSPGC 146

RESULT 4
OB_GORGO
ID OB GORGO STANDARD; PRT; 146 AA.
AC Q95189;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Leptin (Obesity factor).
GN Names=LEP; Synonyms=OB;
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Smith D.P., Zhang X., Hsiung H.M.;
RT "Gorilla leptin genomic sequence.";
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May function as part of a signaling pathway that acts to
CC regulate the size of the body fat depot. An increase in the level
CC of LEP may act directly or indirectly on the CNS to inhibit food
CC intake and/or regulate energy expenditure as part of a homeostatic
CC mechanism to maintain constancy of the adipose mass (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- SIMILARITY: Belongs to the leptin family.
CC
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; U72872; AAB17091.1; -; Genomic_DNA.
CC HSSP; P41159; IAX8.
CC SMR; Q95189; 3-146.
CC InterPro; IPR012351; Cytokine_4_hlx.
CC Panther; PTHR11724; Leptin; 1.
CC Pfam; PF02024; Leptin; 1.
CC PRINTS; PR00495; LEPTIN.
CC ProDom; PD005698; Leptin; 1.
KW Obesity.
FT DISULFID 96 146 By similarity.
SQ SEQUENCE 146 AA; 16031 MW; 02C43BF6B9A4C85C CRC64;

Query Match 98.9%; Score 728; DB 1; Length 146;
Best Local Similarity 98.6%; Pred. No. 4.2e-59;
Matches 144; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 VPIQKVQDDTKLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 1 VPIQKVQDDTKLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

QY 61 YQOILTSMPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
DB 61 YQOILTSMPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYS 120

QY 121 TEVVALSRQGSIQDMLWQLDLSPGC 146
DB 121 TEVVALSRQGSIQDMLWQLDLSPGC 146

RESULT 5
OB_PONPY
ID OB PONPY STANDARD; PRT; 146 AA.
AC Q95234;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Leptin (Obesity factor).
GN Names=LEP; Synonyms=OB;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Schoner B., Basinski M.B., Smith D.P., Heiung H.M., Zhang X.,
RA Rockey P.K., Rosteck P.R.;
RT "Cloning of obese genes from different species: a comparison of the
RT gene structures and the sequences of the obese gene products,
RT leptin.";
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May function as part of a signaling pathway that acts to
CC regulate the size of the body fat depot. An increase in the level
CC of LEP may act directly or indirectly on the CNS to inhibit food
CC intake and/or regulate energy expenditure as part of a homeostatic
CC mechanism to maintain constancy of the adipose mass (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- SIMILARITY: Belongs to the leptin family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; U72873; AAB17092.1; -; Genomic_DNA.
CC HSSP; P41159; IAX8.
CC SMR; Q95234; 3-146.
CC InterPro; IPR012351; Cytokine_4_hlx.
CC Panther; PTHR11724; Leptin; 1.
CC Pfam; PF02024; Leptin; 1.
CC PRINTS; PR00495; LEPTIN.
CC ProDom; PD005698; Leptin; 1.
KW Obesity.
FT DISULFID 96 146 By similarity.
SQ SEQUENCE 146 AA; 16195 MW; 3F50A13338FFDBD4 CRC64;

Query Match 98.0%; Score 721; DB 1; Length 146;
Best Local Similarity 97.3%; Pred. No. 1.9e-58;
Matches 142; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VPIQKVQDDTKLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 1 VPIQKVQDDTKLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

QY 61 YQOILTSMPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
DB 61 YQOILTSMPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
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Db 61 YQQLTSPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLTDLRLGGVLEASGYS 120
QY 121 TEVVALSRLQSLQDMLWQLDLSGCG 146
Db 121 TEVVALSRLQSLQDMLWQLDLSGCG 146

RESULT 6
OB_MACWU
ID_ OB_MACWU STANDARD; PRT; 167 AA.
AC Q28504;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Leptin precursor (Obesity factor).
GN Name=LEP; Synonyms=OB;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OC NCBI_TaxID=9544;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Adipose tissue;
RX MEDLINE=96411743; PubMed=8810296; DOI=10.1074/jbc.271.41.25327;
RA Hotta K., Gustafson T.A., Ortmeier H.K., Bodkin N.L., Nicolson M.A.,
RA Hansen B.C.;
RT "Regulation of obese (ob) mRNA and plasma leptin levels in rhesus
RT monkeys. Effects of insulin, body weight, and non-insulin-dependent
RT diabetes mellitus."
RL J. Biol. Chem. 271:25327-25331(1996).
CC -!- FUNCTION: May function as part of a signaling pathway that acts to
CC regulate the size of the body fat depot. An increase in the level
CC of LEP may act directly or indirectly on the CNS to inhibit food
CC intake and/or regulate energy expenditure as part of a homeostatic
CC mechanism to maintain constancy of the adipose mass.
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- SIMILARITY: Belongs to the leptin family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; U58492; AAC50730.1; -; mRNA.
CC HSP; P41159; IAX8.
CC SMR; Q28504; 24-167.
CC InterPro; IPR012351; Cytokine_4_hlx.
CC PANTHER; PTHR11724; Leptin; 1.
CC Pfam; PF02024; Leptin; 1.
CC PRINTS; PR00495; LEPTIN.
CC ProDom; PD005698; Leptin; 1.
CC Obesity; Signal.
CC SIGNAL 1 21 Potential.
CC CHAIN 22 167 Leptin.
CC DISULFID 117 167 By similarity.
CC SEQUENCE 167 AA; 18953 MW; E7D9F30628A5BBE9 CRC64;

Query Match
Best Local Similarity 91.1%; Score 672; DB 1; Length 167;
Matches 133; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 VPIQKVDQDTKTIKTIIVTRINDISHTQSVSSKQVGTGLDFIPGLHPILTLSKMDQTLAV 60
Db 22 VPIQKVDQDTKTIKTIIVTRINDISHTQSVSSKQVGTGLDFIPGLHPILTLSKMDQTLAI 81

QY 61 YQQLTSPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLTDLRLGGVLEASGYS 120
Db 82 YQQLTSPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLTDLRLGGVLEASGYS 141

QY 121 TEVVALSRLQSLQDMLWQLDLSGCG 146
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Db 142 TEVVALSRLQSLQDMLWQLDLSGCG 167

RESULT 7
OB_FELCA
ID_ OB_FELCA STANDARD; PRT; 167 AA.
AC Q2N2C1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Leptin precursor (Obesity factor).
GN Name=LEP; Synonyms=OB;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC Felinae; Felis.
OC NCBI_TaxID=9685;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=White adipose tissue;
RA Sasaki N., Iwase M., Kimura K., Ohishi I., Saito M.;
RT "Molecular cloning of feline leptin cDNA."
RT Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May function as part of a signaling pathway that acts to
CC regulate the size of the body fat depot. An increase in the level
CC of LEP may act directly or indirectly on the CNS to inhibit food
CC intake and/or regulate energy expenditure as part of a homeostatic
CC mechanism to maintain constancy of the adipose mass (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- SIMILARITY: Belongs to the leptin family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AB0411360; BAA95481.1; -; mRNA.
CC HSP; P41159; IAX8.
CC SMR; Q2N2C1; 24-167.
CC InterPro; IPR012351; Cytokine_4_hlx.
CC PANTHER; PTHR11724; Leptin; 1.
CC Pfam; PF02024; Leptin; 1.
CC PRINTS; PR00495; LEPTIN.
CC ProDom; PD005698; Leptin; 1.
CC Obesity; Signal.
CC SIGNAL 1 21 Potential.
CC CHAIN 22 167 Leptin.
CC DISULFID 117 167 By similarity.
CC SEQUENCE 167 AA; 18584 MW; 643720DBB0A84B95 CRC64;

Query Match
Best Local Similarity 86.8%; Score 639; DB 1; Length 167;
Matches 126; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 VPIQKVDQDTKTIKTIIVTRINDISHTQSVSSKQVGTGLDFIPGLHPILTLSKMDQTLAV 60
Db 22 VPIQKVDQDTKTIKTIIVTRINDISHTQSVSSKQVGTGLDFIPGLHPILTLSKMDQTLAI 81

QY 61 YQQLTSPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLTDLRLGGVLEASGYS 120
Db 82 YQQLTSPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLTDLRLGGVLEASGYS 141

QY 121 TEVVALSRLQSLQDMLWQLDLSGCG 146
Db 142 TEVVALSRLQSLQDMLWQLDLSGCG 167

RESULT 8
Q6T8R8_BUBBU
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ID Q6T8R8 BUBBU PRELIMINARY; PRT; 146 AA.
AC Q6T8R8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Leptin (Fragment).
OS Bubalus bubalis (Domestic water buffalo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bubalus.
OX NCBI_TaxID=89462;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=adipose tissue;
RA Rajendran S., Shukla D.C., Saravanan B.C.;
RT "Cloning and sequencing of buffalo leptin gene.";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
EMBL; AY427959; AAR05862.1; -; mRNA.
DR HSSP; P41159; IAX8.
DR SMR; Q6T8R8; 3-146.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000065; Leptin.
DR Pfam; PF02024; Leptin; 1.
DR PRINTS; PR00495; LEPTIN.
DR ProDom; PD005698; Leptin; 1. leptin.
FT CHAIN <1 146
FT NON_TER 1
SQ SEQUENCE 146 AA; 16069 MW; 1A745EE0851BD8CA CRC64;

Query Match 85.3%; Score 628; DB 2; Length 146;
Best Local Similarity 87.0%; Pred. No. 7.1e-50;
Matches 127; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 VPIKQVDDPTLIKIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 VPIKQVDDPTLIKIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAI 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 YQILTSMPNRVNIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSIGGVLEASGVY 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 YQILTSMPNRVNIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSIGGVLEASLVY 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 TEVVALSRLOGLQDMLWLDLSPGC 146
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 TEVVALSRLOGLQDMLWLDLSPGC 146
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
OB_BOVIN STANDARD; PRT; 167 AA.
AC P50595; Q97918; Q95133; Q9TS29;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Leptin precursor (Obesity factor).
GN Names=LEP; Synonyms=OB, OBS;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RA Tellam R.L., Briscoe S., Vuocolo A.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE OF 22-167.
RA Ji S., Spurlock M.E.;
RT "Partial cloning of bovine obesity gene.";
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE OF 22-167.
RC TISSUE=White adipose tissue;
RA Kawakita Y., Abe H., Miyashige T.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE, AND VARIANTS CYS-25 AND VAL-80.
RC STRAIN=Jersey;
RX MEDLINE=20063685; PubMed=10594237; DOI=10.1007/s003359901180;
RA Konfortov B.A., Licence V.E., Miller J.R.;
RT "Resequencing of DNA from a diverse panel of cattle reveals a high
level of polymorphism in both intron and exon.";
RN Mamm. Genome 10:1142-1145(1999).
RN [5]
RP NUCLEOTIDE SEQUENCE, AND VARIANT CYS-25.
RA Liefers S.C.;
RT "Genotype effects of bovine leptin mutations on pre- and postpartum
leptin concentrations.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE OF 46-145.
RA Lien S., Sundvold H., Klungland H., Vaage D.I.;
RT "Two novel polymorphisms in the bovine obesity gene (OBS).";
RN Anim. Genet. 28:245-245(1997).
RN [7]
RP NUCLEOTIDE SEQUENCE OF 60-146.
RX MEDLINE=96269621; PubMed=8661738; DOI=10.1007/s003359900118;
RA Pfister-Genskow M.A., Hayes H., Eggen A., Bishop M.D.;
RT "Chromosomal localization of the bovine obesity (OBS) gene.";
RN Mamm. Genome 7:398-399(1996).
RN [8]
RP NUCLEOTIDE SEQUENCE OF 1-48.
RA Fitzsimmons C.J., Schmitz S.M.;
RT "Exon two of the bovine obese, leptin, gene.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May function as part of a signaling pathway that acts to
regulate the size of the body fat depot. An increase in the level
of LEP may act directly or indirectly on the CNS to inhibit food
intake and/or regulate energy expenditure as part of a homeostatic
mechanism to maintain constancy of the adipose mass.
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- SIMILARITY: Belongs to the leptin family.
CC -----
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use as long as its content is in no way modified and this statement is not
removed.
CC -----
DR EMBL; U43943; AAA85906.1; -; mRNA.
DR EMBL; U50365; AAB61244.1; -; Genomic_DNA.
DR EMBL; U65793; AAB06579.1; -; mRNA.
DR EMBL; AB003143; BAA19750.1; -; mRNA.
DR EMBL; AJ132764; CAB64255.1; -; Genomic DNA.
DR EMBL; AJ236854; CAB38018.1; -; Genomic DNA.
DR EMBL; AJ512638; CAD54745.1; -; Genomic DNA.
DR EMBL; AJ512639; CAD54745.1; JOINED; Genomic_DNA.
DR EMBL; Y11369; CAA72197.1; -; Genomic_DNA.
DR EMBL; U43833; AAB18762.1; -; Genomic_DNA.
DR EMBL; AF10500; AAD23567.1; -; Genomic_DNA.
DR HSSP; P41159; IAX8.
DR SMR; P50595; 24-167.
DR InterPro; IPR012351; Cytokine_4_hlx.
DR InterPro; IPR000065; Leptin.
DR PANTHER; PTHR11724; Leptin; 1.
DR Pfam; PF02024; Leptin; 1.
DR PRINTS; PR00495; LEPTIN.
DR ProDom; PD005698; Leptin; 1.
KW Obesity; Polymorphism; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 167 Leptin.
FT DISULFID 117 167 By similarity.
FT VARIANT 25 25 R -> C.
FT VARIANT 80 80 A -> V.

```

```
FT CONFLICT 25 25 R -> Q (in Ref. 2).
FT CONFLICT 166 166 G -> E (in Ref. 2).
SQ SEQUENCE 167 AA; 18716 MW; 94C666B3069E50B7 CRC64;

Query Match 85.3%; Score 628; DB 1; Length 167;
Best Local Similarity 87.0%; Pred. No. 8.3e-50;
Matches 127; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

Qy 1 VPIQKQVDDTKTLIKTIIVTRINDISHTSQSSKQVGTGLDPIPGHLPILTLISKMDQTLAV 60
Db 22 VPIKQVDDTKTLIKTIIVTRINDISHTSQSSKQVGTGLDPIPGHLPILTLISKMDQTLAI 81
Qy 61 YQILTSMPNRNVQISNDLENLRLDHLHVLAFPSKCHLPWASGLTLDLSLGGVLEASGYS 120
Db 82 YQILTSMPNRNVQISNDLENLRLDHLHVLAFPSKCHLPWASGLTLDLSLGGVLEASGYS 141
Qy 121 TEVALSRLOGLQDMLWQLDLSFGC 146
Db 142 TEVALSRLOGLQDMLRQLDLSFGC 167

RESULT 10
OB_BUBBU STANDARD; PRT; 167 AA.
AC Q5J732;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Leptin precursor (Obesity factor).
GN Name=LEP; Synonyms=OB;
OS Bubalus bubalis (Domestic water buffalo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bubalus.
OX NCBI_TaxID=89462;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA PubMed=15566470; DOI=10.1111/j.1365-2052.2004.01186.x;
RA Vallinoto M., Schneider M.P., Silva A., Iannuzzi L., Brenig B.;
RT "Molecular cloning and analysis of the swamp and river buffalo leptin gene.";
RT Anim. Genet. 35:462-463(2004).
CC -!- FUNCTION: May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of LEP may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintain constancy of the adipose mass (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- SIMILARITY: Belongs to the leptin family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC -----
DR EMBL; AY495587; AAC86311.1; -; Genomic DNA.
DR SMR; Q5J732; 24-167.
DR InterPro; IPR012351; Cytokine_4_hlx.
DR InterPro; IPR000065; Leptin.
DR PANTHER; PTHR11724; Leptin; 1.
DR Pfam; PF02024; Leptin; 1.
DR PRINTS; PR00495; LEPTIN.
DR ProDom; PD005698; Leptin; 1.
DR Obesity; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 167 Leptin.
FT DISULFID 117 167 By similarity.
SQ SEQUENCE 167 AA; 18688 MW; 8524749CD69CAD99 CRC64;

Query Match 85.3%; Score 628; DB 1; Length 167;
Best Local Similarity 87.0%; Pred. No. 8.3e-50;
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Qy 61 YQILTSMPNRNVQISNDLENLRLDHLHVLAFPSKCHLPWASGLTLDLSLGGVLEASGYS 120
Db 82 YQILTSMPNRNVQISNDLENLRLDHLHVLAFPSKCHLPWASGLTLDLSLGGVLEASGYS 141
Qy 121 TEVALSRLOGLQDMLWQLDLSFGC 146
Db 142 TEVALSRLOGLQDMLRQLDLSFGC 167

RESULT 11
OB_PIG STANDARD; PRT; 167 AA.
AC Q29406; O19095; Q95251;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Leptin precursor (Obesity factor).
GN Name=LEP; Synonyms=OB; OBS;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Adipose tissue;
RA Louis C.F.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Ramsay T.G., Yan X.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Landrace;
RA Robert C., Falin M.-F., Coulombe N., Roberge C., Silversides F.G., Benkel B.F., McKay R.M., Pelletier G.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Bidwell C.A., Ji S., Spurlock M.E.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Meishan;
RA Dai R., Li N., Hu X., Wu C.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RA McNeel R.L., Mersmann H.J.;
RT "Adipose tissue regulatory transcript expression in lean versus obese pigs.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Large white;
RA Soares M.A.M., Euclydes R.F., Guimaraes S.E.F., Martins M.F., Lopes P.S.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [8]
RP NUCLEOTIDE SEQUENCE OF 15-110.
RC TISSUE=White adipose tissue;
RX MEDLINE=97009821; PubMed=8856925;
RA Neuenchwander S., Rettenberger G., Meijerink E., Jorg H., Stranzinger G.;
RT "Partial characterization of porcine obesity gene (OBS) and its localization to chromosome 18 by somatic cell hybrids.";
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC -----
DR EMBL; U84247; AAB41786.1; -; mRNA.
DR EMBL; U62123; AAB51033.1; -; mRNA.
DR HSSP; P41159; IAX8.
DR SMR; Q28603; 3-146.
DR InterPro; IPR012351; Cytochrome_4_hlx.
DR PANTHER; PTHR11724; Leptin; 1.
DR Pfam; PF02024; Leptin; 1.
DR PRINTS; PR00495; LEPTIN.
DR ProDom; PD005698; Leptin; 1.
KW Obesity.
FT DISULFID 96 146 By similarity.
FT CONFLICT 65 65 L -> H (in Ref. 2).
FT CONFLICT 92 92 A -> G (in Ref. 2).
FT CONFLICT 124 124 V -> L (in Ref. 2).
SQ SEQUENCE 146 AA; 16054 MW; 19D54C53240968CA CRC64;

Query Match 84.8%; Score 624; DB 1; Length 146;
Best Local Similarity 87.0%; Pred. No. 1.6e-49;
Matches 127; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

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Qy 61 YQILTSMPSPNRVQISNDLENLRLDLHLVAFSKCHLPWASGLTLDLSLGGVLEASGYS 120
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RESULT 14

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AC Q5EAE4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Leptin.
GN Name=LEP;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pooled;
RX MEDLINE=21180013; PubMed=11282978; DOI=10.1101/gr.170101;
RA Smith T.P.L., Grosse W.M., Fraking B.A., Roberts A.J., Stone R.T.,
RA Casas E., Wray J.E., White J., Cho J., Fahrkrug S.C., Bennett G.L.,
RA Heaton M.P., Laegreid W.W., Rohrer G.A., Chitko-McKown C.G.,
RA Pertea G., Holt I., Karamycheva S., Liang F., Quackenbush J.,
RA Keele J.W.;
RT "Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle.";
RL Genome Res. 11:626-630(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pooled;
RA Hathay G.P., Sonategard T.S., Clawson M.L., Heaton M.P., Keele J.W.,
RA Snelling W.M., Weidmann R.T., Smith T.P.L.;
RT "Sequencing and analysis of Bos taurus full-length insert cDNA
clones.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT020625; AAX08642.1; -; mRNA.

DR SMR; Q5EAE4; 24-167.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000065; Leptin.
DR Pfam; PF02024; Leptin; 1.
DR PRINTS; PR00495; LEPTIN.
SQ SEQUENCE 167 AA; 18663 MW; C9AA16B31AF229CE CRC64;

Query Match 84.8%; Score 624; DB 2; Length 167;
Best Local Similarity 87.0%; Pred. No. 1.9e-49;
Matches 127; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

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Qy 61 YQILTSMPSPNRVQISNDLENLRLDLHLVAFSKCHLPWASGLTLDLSLGGVLEASGYS 120
Db 82 YQILTSMPSPNRVQISNDLENLRLDLHLVAFSKCHLPWASGLTLDLSLGGVLEASLYS 141
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Db 142 TEVALSRLOGLQDMLRQLDLSGPC 167

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DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Obese protein (Fragment).
OS Ctenopharyngodon idella (Grass carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Ctenopharyngodon.
OX NCBI_TaxID=7959;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mesentery adipose tissue;
RA Dai H., Long L.;
RT "Molecular cloning and sequence analysis of the obese gene from the
Ctenopharyngodon idellus.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY551335; AAT45394.1; -; mRNA.
FT NON_TER 1
SQ SEQUENCE 146 AA; 16004 MW; 60D1A3BF6EB062AB CRC64;

Query Match 84.1%; Score 619; DB 2; Length 146;
Best Local Similarity 84.9%; Pred. No. 4.8e-49;
Matches 124; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

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Job time : 146.498 secs

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GenCore version 5.1.7
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364.525 Million cell updates/sec

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Perfect score: 736
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	736	100.0	146	1	US-08-398-021-3 Sequence 3, Appli
2	736	100.0	146	1	US-08-788-943A-5 Sequence 5, Appli
3	736	100.0	146	1	US-08-823-104-3 Sequence 3, Appli
4	736	100.0	146	1	US-09-003-081-6 Sequence 6, Appli
5	736	100.0	146	2	US-08-648-262-6 Sequence 6, Appli
6	736	100.0	146	2	US-08-648-263-6 Sequence 32, Appli
7	736	100.0	146	2	US-08-914-375C-32 Sequence 1, Appli
8	736	100.0	146	2	US-09-172-644-1 Sequence 1, Appli
9	736	100.0	146	2	US-09-221-178-1 Sequence 1, Appli
10	736	100.0	146	2	US-09-200-919-1 Sequence 2, Appli
11	736	100.0	146	4	PCT-US96-00952-2 Sequence 2, Appli
12	736	100.0	146	4	PCT-US96-00952-3 Sequence 3, Appli
13	736	100.0	147	2	US-09-200-919-4 Sequence 4, Appli
14	736	100.0	148	1	US-08-429-362-3 Sequence 3, Appli
15	736	100.0	148	1	US-08-823-104-18 Sequence 18, Appli
16	736	100.0	167	1	US-08-540-242A-4 Sequence 4, Appli
17	736	100.0	167	1	US-08-347-563A-4 Sequence 4, Appli
18	736	100.0	167	1	US-09-003-081-5 Sequence 5, Appli
19	736	100.0	167	2	US-08-292-345B-6 Sequence 4, Appli
20	736	100.0	167	2	US-08-648-262-5 Sequence 5, Appli
21	736	100.0	167	2	US-08-648-263-5 Sequence 5, Appli
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35	736	100.0	167	2	US-09-686-647A-4 Sequence 4, Appli
36	736	100.0	167	4	PCT-US96-01471-4 Sequence 4, Appli
37	736	100.0	374	2	US-10-679-999-15 Sequence 15, Appli
38	736	100.0	374	2	US-10-679-999-18 Sequence 18, Appli
39	736	100.0	379	2	US-10-679-999-9 Sequence 9, Appli
40	736	100.0	379	2	US-10-679-999-12 Sequence 12, Appli
41	736	100.0	397	2	US-10-775-066-2 Sequence 2, Appli
42	733	99.6	146	2	US-08-914-375C-34 Sequence 34, Appli
43	731	99.3	146	1	US-08-788-943A-2 Sequence 2, Appli
44	731	99.3	146	1	US-08-788-943A-3 Sequence 3, Appli
45	731	99.3	146	1	US-08-823-104-11 Sequence 11, Appli

ALIGNMENTS

RESULT 1
US-08-398-021-3
; Sequence 3, Application US/08398021
; Patent No. 5594101
; GENERAL INFORMATION:
; APPLICANT: Becker, Gerald W.
; APPLICANT: Hale, John E.
; APPLICANT: MacKellar 1, Warren C.
; TITLE OF INVENTION: ANTI-OBESITY PROTEINS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center/Patent Division
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/398,021
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Caltrider, Steven P.
; REGISTRATION NUMBER: 36,467
; REFERENCE/DOCKET NUMBER: X10001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-277-0757
; TELEFAX: 317-277-1917
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-398-021-3

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FEATURE:
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US-08-823-104-3

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Best Local Similarity 100.0%; Pred. No. 3.4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 121 TEVALSRLOGLQSLQDMLWQLDLSPEC 146

RESULT 4
US-09-003-081-6
; Sequence 6, Application US/09003081
; Patent No. 5968779
; GENERAL INFORMATION:
; APPLICANT: Campfield, Arthur Dr.
; APPLICANT: Devos, Rene Dr.
; APPLICANT: Guisez, Yves Dr.
; TITLE OF INVENTION: Recombinant Obese (OB) Proteins
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche, Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/003,081
; FILING DATE:

CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/435,777
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Picot, Catherine A.
REGISTRATION NUMBER: 37419
REFERENCE/DOCKET NUMBER: 9165
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-4387
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-003-081-6
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Best Local Similarity 100.0%; Pred. No. 3.4e-74;
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Db 121 TEVALSRLOGLQSLQDMLWQLDLSPEC 146
RESULT 5
US-08-648-262-6
; Sequence 6, Application US/08648262
; Patent No. 6025324
; GENERAL INFORMATION:
; APPLICANT: Bailon, Pascal Mr.
; APPLICANT: Campfield, Arthur Dr.
; APPLICANT: Devos, Rene Dr.
; APPLICANT: Guisez, Yves Dr.
; TITLE OF INVENTION: Pegylated Obese (OB) Proteins
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche, Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/648,262
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Epstein, William H.
; REGISTRATION NUMBER: 20008
; REFERENCE/DOCKET NUMBER: 9281
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-3723
; TELEFAX: (201) 235-2363

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; TOPOLOGY: unknown
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; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-648-262-6

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Best Local Similarity 100.0%; Pred. No. 3.4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Db 1 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Qy 61 YQOILTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
Db 61 YQOILTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
Qy 121 TEVVALSRQGSQDMLWQLDLSPGC 146
Db 121 TEVVALSRQGSQDMLWQLDLSPGC 146

RESULT 6
US-08-648-263-6
; Sequence 6, Application US/08648263
; Patent No. 6025325
; GENERAL INFORMATION:
; APPLICANT: Campfield, Arthur
; APPLICANT: Devos, Rene
; APPLICANT: Guisez, Yves
; TITLE OF INVENTION: RECOMBINANT OBESE (OB) PROTEINS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingeland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/648,263
; FILING DATE: 15-MAY-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,629
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/435,777
; FILING DATE: 05-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kreieler, Lewis J
; REGISTRATION NUMBER: 38522
; REFERENCE/DOCKET NUMBER: RAN 4105/175-002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201)235-4387
; TELEFAX: (201) 235-2363
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: unknown
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; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-648-263-6

Query Match      100.0%; Score 736; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 3.4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Db 1 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Qy 61 YQOILTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
Db 61 YQOILTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
Qy 121 TEVVALSRQGSQDMLWQLDLSPGC 146
Db 121 TEVVALSRQGSQDMLWQLDLSPGC 146

RESULT 7
US-08-914-375C-32
; Sequence 32, Application US/08914375C
; Patent No. 6377893
; GENERAL INFORMATION:
; APPLICANT: Steven A. Benner
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven A. Benner
; STREET: 1501 NW 68th Terrace
; CITY: Gainesville
; STATE: FL
; COUNTRY: United States
; ZIP: 32605-4147
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/914,375C
; FILING DATE: 19-Aug-1997
; CLASSIFICATION: 702/20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 352 392 7773
; TELEFAX: 352 331 0462
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; OTHER INFORMATION: leptin
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
; US-08-914-375C-32

Query Match      100.0%; Score 736; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 3.4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Db 1 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Qy 61 YQOILTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
Db 61 YQOILTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
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db 61 YQOILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDLSGGVLEASGYS 120

OV 121 TEVALSRQSLQDMLWQDLSPGC 146

db 121 TEVALSRLOGSL0DMLW0LDLSPGC 146

RESULT 10

RESULTS TO
US-09-200-919-1

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US-09-200-919-1
; Sequence 1, Application US/09200919
; Patent No. 6518235
; GENERAL INFORMATION:
; APPLICANT: OOMURA, YUTAKA
; APPLICANT: HORI, NOBUAKI
; APPLICANT: SHIRAISHI, TAKEMASA
; APPLICANT: SASAKI, KAZUO
; APPLICANT: TAKEDA, HIROSHI
; APPLICANT: TSUJII, MINORU
; APPLICANT: MATSUMIYA, TOSHIHIKO
; TITLE OF INVENTION: DRUG FOR IMPROVEMENT OF BRAIN FUNCTION
; FILE REFERENCE: YAMA-100
; CURRENT APPLICATION NUMBER: US/09/200.919
; CURRENT FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 146
; TYPE: PRT
; ORGANISM: HUMAN
US-09-200-919-1

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Query Match	100.0%	Score 736;	DB 2;	Length 146;
Best Local Similarity	100.0%;	Pred. NO. 3.4e-74;		
Matches 146.	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

1 VPIOKVODPTKTLIXTIVTRINDISHTOSVSSKOKVTGLDFIPGLHPILTLSKMDQTLAV 60

1 YPIAK/ODDTKI.I KTI VTB INDI SHTO SVSSKOKVTGI.DET PGI HPILTI.SKMPOTLAV 60

61 YQOTI.TSMPSRNVIOISNDLENLRDILLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120

61 YOOII.TSMPSRNVIOISNDI.ENT.RDI.I.HVT.AFSKSCHL.PWASGLETLDLSGGVLEASGYS 120

121 TEVVAISRI,OGSLODMLWOLDLSPGC 146

121 TEWAI SPLOCSLODWT.WOLDI.SPCC 146

DEPTH 11

RESULT 11
DCT-11806-00053-3

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PCT-US96-00952-2
; sequence 2, Application PC/TUS9600952
; GENERAL INFORMATION:
;
; APPLICANT:
;
; TITLE OF INVENTION: Anti-Obesity Proteins
;
; NUMBER OF SEQUENCES: 16
;
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: PCT/US96/00952
;
; FILING DATE:
;
; CLASSIFICATION:
;
; INFORMATION FOR SEQ ID NO: 2:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 146 amino acids
;
; TYPE: amino acid
;
; STRANDEDNESS: single
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: protein
;
; PCT-US96-00952-2

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Ov 121 TEVVALSRLOGSLDMLWOLDLSPGC 146

db 121 TEVVALSRLOGSLQDMLWOLDLSPGC 146

RESIST. T. 8

RESULTS 8
IIS-09-172-644-1

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US-09-172-644-1
; Sequence 1, Application US/09172644
; Patent No. 6420339
; GENERAL INFORMATION:
; APPLICANT: GEGG, COLIN
; APPLICANT: KINSTLER, OLAF
; TITLE OF INVENTION: SITE-DIRECTED DUAL PEGYLATION OF PROTEINS FOR IMPROVED
; TITLE OF INVENTION: BIOACTIVITY AND BIOCOMPATIBILITY
; FILE REFERENCE: A-567
; CURRENT APPLICATION NUMBER: US/09/172,644
; CURRENT FILING DATE: 1998-10-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Human Leptin
US-09-172-644-1

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Query Match	100.0%	Score 736;	DB 2;	Length 146;
Best Local Similarity	100.0%;	Pred. No. 3.4e-74;		
Matches 146.	Conservative	0;	Mismatches 0;	Indels 0;
				Gaps 0;

0V 1 VPIOKVODPTKTLIKTIVTRINDISHTOSVSSKOKVTGLDFIPGLHPILTLSKMDOTLAV 60

1 VPIK/VONDTKTI.IKTIYTB INDI SHTOSVSSKOKVTGI.DET PGI.HPTI.TI.SKMDOTI.AV 60

61 YOOTLTSMPSRNVIOISNDI.ENIRDI.HVLA.PSKSCHIPWASGI.ETLDSLGGVLEASGYS 120

61 YOCII TTEMPEPNTIO I SNDI ENI PNI I HVI AFSKVSCHI PWASCI ETI DSI GGVI EASGVS 120

121 TEWALSPICST.ODMT.WOL.DI.SPCC 146

n

121 TTTTATLSPILQCSLODMLWOLDSRCC 146

DATE

RESULT 9
IIS-08-221-178-1

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US-09-221-178-1
; Sequence 1, Application US/09221178
; Patent No. 6451346
; GENERAL INFORMATION:
; APPLICANT: SHAH, SUBODH
; APPLICANT: DAI, WEIGUO
; TITLE OF INVENTION: BIODEGRADABLE, pH/THERMOSENSITIVE HYDROGEL FOR
; SUSTAINED DELIVERY OF BIOLOGICALLY ACTIVE AGENTS
; FILE REFERENCES: A-575
; CURRENT APPLICATION NUMBER: US/09/221,178
; CURRENT FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Human Leptin
; US-09-221-178-1

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Query Match	100.0%	Score 736;	DB 2;	Length 146;
Best Local Similarity	100.0%	Pred. No. 3.4e-74;		
Matches 146; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

Qz 1 VP1OKVONDTKTI.IKTIYTRINDISHTQSVSSKOKVTGLDFIPGLHPILTL SKMDOTLAV 60

1 VDOT/CV/ORDT/KYI I WTT/IMP INDI SUH/TAS/VSS/KAT/CI DEIR/GI/HPI/I.TI.SKMDOT/LAY 60

51 YOOII TSMPSNVIOTISNDIENIRDLIHWI AFKSKSCHLPWASGL ETI DSI GGV EASGYS 120

Query Match 100.0%; Score 736; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 3.4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
DB 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
QY 61 YQILTSMPSRNVQISNDLENRLDLHLVLAFSKCHLPWASGLETLDSLGGLVLEASGYS 120
DB 61 YQILTSMPSRNVQISNDLENRLDLHLVLAFSKCHLPWASGLETLDSLGGLVLEASGYS 120
QY 121 TEVVALSRQGSQDMLWQDLSPGC 146
DB 121 TEVVALSRQGSQDMLWQDLSPGC 146

RESULT 12

PCT-US96-00952-3

; Sequence 3, Application PC/TUS9600952

; GENERAL INFORMATION:

; APPLICANT: Anti-Obesity Proteins

; TITLE OF INVENTION: Anti-Obesity Proteins

; NUMBER OF SEQUENCES: 16

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US96/00952

; FILING DATE:

; CLASSIFICATION:

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 146 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; PCT-US96-00952-3

Query Match 100.0%; Score 736; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 3.4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
DB 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
QY 61 YQILTSMPSRNVQISNDLENRLDLHLVLAFSKCHLPWASGLETLDSLGGLVLEASGYS 120
DB 61 YQILTSMPSRNVQISNDLENRLDLHLVLAFSKCHLPWASGLETLDSLGGLVLEASGYS 120
QY 121 TEVVALSRQGSQDMLWQDLSPGC 146
DB 121 TEVVALSRQGSQDMLWQDLSPGC 146

RESULT 13

US-09-200-919-4

; Sequence 4, Application US/09200919

; Patent No. 6518235

; GENERAL INFORMATION:

; APPLICANT: OOMURA, YUTAKA

; APPLICANT: HORI, NOBUAKI

; APPLICANT: SHIRAI, TAKEMASA

; APPLICANT: SASAKI, KAZUO

; APPLICANT: TAKEDA, HIROSHI

; APPLICANT: TSUJI, MINORU

; APPLICANT: MATSUMIYA, TERUHIKO

; TITLE OF INVENTION: DRUG FOR IMPROVEMENT OF BRAIN FUNCTION

; FILE REFERENCE: YAMA-100

; CURRENT APPLICATION NUMBER: US/09/200,919
; CURRENT FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 147
; TYPE: PRP
; ORGANISM: HUMAN
US-09-200-919-4

Query Match 100.0%; Score 736; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 3.5e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
DB 2 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 61
QY 61 YQILTSMPSRNVQISNDLENRLDLHLVLAFSKCHLPWASGLETLDSLGGLVLEASGYS 120
DB 62 YQILTSMPSRNVQISNDLENRLDLHLVLAFSKCHLPWASGLETLDSLGGLVLEASGYS 121
QY 121 TEVVALSRQGSQDMLWQDLSPGC 146
DB 122 TEVVALSRQGSQDMLWQDLSPGC 147

RESULT 14

US-08-429-362-3

; Sequence 3, Application US/08429362

; Patent No. 5614379

; GENERAL INFORMATION:

; APPLICANT: Mackellar, Warren C.

; TITLE OF INVENTION: Process For Preparing Anti-Obesity

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Eli Lilly and Company/Patent Division

; STREET: Lilly Corporate Center

; CITY: Indianapolis

; STATE: Indiana

; COUNTRY: United States

; ZIP: 46285

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/429,362

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Caltrider, Steven P.

; REGISTRATION NUMBER: 36,467

; REFERENCE/DOCKET NUMBER: X10022

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (317) 276-0757

; TELEFAX: (317) 277-1917

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 148 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-429-362-3

Query Match 100.0%; Score 736; DB 1; Length 148;
Best Local Similarity 100.0%; Pred. No. 3.5e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60

Db 3 VPIQKQDDTKTLIKTIIVTRINDISHQTSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 62
QY 61 YQQLTSMPSRNVQISNDLENRLDLHLVLAFSKCHLPWASGLETLDSLGGVLEASGYS 120
Db 63 YQQLTSMPSRNVQISNDLENRLDLHLVLAFSKCHLPWASGLETLDSLGGVLEASGYS 122
QY 121 TEVVLSRQSGSLQDMLWQLDLSFGC 146
Db 123 TEVVLSRQSGSLQDMLWQLDLSFGC 148

QY 121 TEVVLSRQSGSLQDMLWQLDLSFGC 146
Db 123 TEVVLSRQSGSLQDMLWQLDLSFGC 148
Search completed: May 4, 2006, 21:58:25
Job time : 34.1134 secs

RESULT 15
US-08-823-104-18
; Sequence 18, Application US/08823104
; Patent No. 5840517
; GENERAL INFORMATION:
; APPLICANT: Atkinson, Paul R
; APPLICANT: Foster, Lisa K
; APPLICANT: Furman, Thomas C
; APPLICANT: MacKellar, Warren C
; TITLE OF INVENTION: Process for Preparing Obesity Protein
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly & Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/823,104
; FILING DATE: 24-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/429,362
; FILING DATE: 26-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Caltrider, Steven P
; REGISTRATION NUMBER: 36467
; REFERENCE/DOCKET NUMBER: 10022A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-277-8110
; TELEFAX: 317-277-1917
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 148 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-823-104-18

Query Match 100.0%; Score 736; DB 1; Length 148;
Best Local Similarity 100.0%; Pred. No. 3.5e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPIQKQDDTKTLIKTIIVTRINDISHQTSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Db 3 VPIQKQDDTKTLIKTIIVTRINDISHQTSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 62
QY 61 YQQLTSMPSRNVQISNDLENRLDLHLVLAFSKCHLPWASGLETLDSLGGVLEASGYS 120
Db 63 YQQLTSMPSRNVQISNDLENRLDLHLVLAFSKCHLPWASGLETLDSLGGVLEASGYS 122

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 4, 2006, 21:57:29 ; Search time 112.887 Seconds
(without alignments)
540.393 Million cell updates/sec

Title: US-10-623-189-1

Perfect score: 736

Sequence: 1 VPIQKVDDTKTLIKTIVTR.....SRQGSIQDMLWQLDLSPGC 146

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	736	100.0	146	4	US-10-139-794-10
3	736	100.0	146	4	US-10-419-058-2
4	736	100.0	146	4	US-10-467-114-1
5	736	100.0	146	4	US-10-622-998-1
6	736	100.0	146	4	US-10-658-834A-211
7	736	100.0	146	4	US-10-468-496-1
8	736	100.0	146	5	US-10-872-198-127
9	736	100.0	146	5	US-10-623-189-1
10	736	100.0	146	5	US-10-502-344-22
11	736	100.0	146	6	US-11-021-951-127
12	736	100.0	167	3	US-09-736-084-4
13	736	100.0	167	3	US-09-928-522-7
14	736	100.0	167	3	US-09-789-306-3
15	736	100.0	167	3	US-09-804-409A-11
16	736	100.0	167	3	US-09-316-393-4
17	736	100.0	167	4	US-10-440-464-67
18	736	100.0	167	4	US-10-458-334-17
19	736	100.0	167	4	US-10-730-488-4
20	736	100.0	167	4	US-10-780-295-4
21	736	100.0	167	5	US-10-723-860-2482
22	736	100.0	167	5	US-10-698-510-17
23	736	100.0	167	5	US-10-775-180-168
24	736	100.0	167	5	US-10-775-180-169
25	736	100.0	167	5	US-10-775-180-170
26	736	100.0	167	5	US-10-775-180-171
27	736	100.0	167	5	US-10-893-315-63

28 736 100.0 167 5 US-10-756-149-5381 Sequence 5381, App
29 736 100.0 167 5 US-10-775-204-551 Sequence 551, App
30 736 100.0 167 5 US-10-775-204-555 Sequence 555, App
31 736 100.0 167 5 US-10-775-204-557 Sequence 557, App
32 736 100.0 167 5 US-10-775-204-558 Sequence 558, App
33 736 100.0 167 6 US-11-060-291-1 Sequence 1, Appli
34 736 100.0 171 5 US-10-908-400A-105 Sequence 105, App
35 736 100.0 178 5 US-10-893-315-108 Sequence 108, App
36 736 100.0 374 4 US-10-679-999-15 Sequence 15, Appl
37 736 100.0 374 4 US-10-679-999-18 Sequence 18, Appl
38 736 100.0 374 6 US-11-054-085-15 Sequence 15, Appl
39 736 100.0 374 6 US-11-054-085-18 Sequence 18, Appl
40 736 100.0 379 4 US-10-679-999-9 Sequence 9, Appli
41 736 100.0 379 4 US-10-679-999-12 Sequence 12, Appl
42 736 100.0 379 6 US-11-054-085-9 Sequence 9, Appli
43 736 100.0 379 6 US-11-054-085-12 Sequence 12, Appl
44 736 100.0 396 3 US-09-859-361-2 Sequence 2, Appli
45 736 100.0 396 3 US-09-859-361-5 Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-10-191-377-1

; Sequence 1, Application US/10191377

; Publication No. US20030099709A1

; GENERAL INFORMATION:

; APPLICANT: AMGEN INC.

; TITLE OF INVENTION: BIODEGRADABLE, PH/THERMOSENSITIVE HYDROGEL FOR

; FILE REFERENCE: A-575

; CURRENT APPLICATION NUMBER: US/10/191.377

; CURRENT FILING DATE: 1998-12-23

; NUMBER OF SEQ ID NOS: 1

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 146

; TYPE: PRT

; ORGANISM: Human Leptin

US-10-191-377-1

Query Match 100.0%; Score 736; DB 4; Length 146;

Best Local Similarity 100.0%; Pred. No. 4.3e-72;

Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVDDTKTLIKTIVTRINDISHTSQSVSSKOKVTGLDLPFGHLPIITLSKMDQTLAV 60
Db 1 VPIQKVDDTKTLIKTIVTRINDISHTSQSVSSKOKVTGLDLPFGHLPIITLSKMDQTLAV 60
Qy 61 YQQILTSPSRNVQISNDLENLRLDLHLVLAFSKLSCHLPWASGLTDLDSLGVLASGYS 120
Db 61 YQQILTSPSRNVQISNDLENLRLDLHLVLAFSKLSCHLPWASGLTDLDSLGVLASGYS 120
Qy 121 TEVVALSRQGSIQDMLWQLDLSPGC 146
Db 121 TEVVALSRQGSIQDMLWQLDLSPGC 146

RESULT 2

US-10-139-794-10

; Sequence 10, Application US/10139794

; Publication No. US20030232421A1

; GENERAL INFORMATION:

; APPLICANT: HYBRIGENICS, LYNX THERAPEUTICS INC.

; APPLICANT: Pierre Legrain, Simon Whiteside, Jen-I Mao, Irina Khrebtukova, Shujun

; TITLE OF INVENTION: Protein-Protein Interactions in Adipocyte Cells (3)

; FILE REFERENCE: B4883A

; CURRENT APPLICATION NUMBER: US/10/139,794

; CURRENT FILING DATE: 2002-05-06

; PRIOR APPLICATION NUMBER: US 60/288,885

; PRIOR FILING DATE: 2001-05-04

; NUMBER OF SEQ ID NOS: 2930

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: Translation of SEQ ID NO:9
US-10-139-794-10

Query Match      100.0%; Score 736; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.3e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

QY 61 YQILTMPSRNVQISNDLENLRLDLHLVLAFAFKSCHLPWASGLETLDSLGGLVLEASGYS 120
DB 61 YQILTMPSRNVQISNDLENLRLDLHLVLAFAFKSCHLPWASGLETLDSLGGLVLEASGYS 120

QY 121 TEVVLSRLQGSQDMLWQLDLSPGC 146
DB 121 TEVVLSRLQGSQDMLWQLDLSPGC 146

RESULT 3
US-10-419-058-2
; Sequence 2, Application US/10419058
; Publication No. US20040053366A1
; GENERAL INFORMATION:
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Zhang, Jinyang
; TITLE OF INVENTION: Expression and Export of Anti-Obesity Proteins as Fc
; TITLE OF INVENTION: Fusion Proteins
; FILE REFERENCE: LEX-008
; CURRENT APPLICATION NUMBER: US/10/419,058
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: US/09/479,508
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 60/115,079
; PRIOR FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 2
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-419-058-2

Query Match      100.0%; Score 736; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.3e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

QY 61 YQILTMPSRNVQISNDLENLRLDLHLVLAFAFKSCHLPWASGLETLDSLGGLVLEASGYS 120
DB 61 YQILTMPSRNVQISNDLENLRLDLHLVLAFAFKSCHLPWASGLETLDSLGGLVLEASGYS 120

QY 121 TEVVLSRLQGSQDMLWQLDLSPGC 146
DB 121 TEVVLSRLQGSQDMLWQLDLSPGC 146

RESULT 4
US-10-467-114-1
; Sequence 1, Application US/10467114
; Publication No. US20040072219A1
; GENERAL INFORMATION:
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; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: MODIFIED LEPTIN WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-115
; CURRENT APPLICATION NUMBER: US/10/467,114
; CURRENT FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: EP 01102618.4
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: EP 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: PCT/EP02/01188
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-467-114-1

Query Match      100.0%; Score 736; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.3e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

QY 61 YQILTMPSRNVQISNDLENLRLDLHLVLAFAFKSCHLPWASGLETLDSLGGLVLEASGYS 120
DB 61 YQILTMPSRNVQISNDLENLRLDLHLVLAFAFKSCHLPWASGLETLDSLGGLVLEASGYS 120

QY 121 TEVVLSRLQGSQDMLWQLDLSPGC 146
DB 121 TEVVLSRLQGSQDMLWQLDLSPGC 146

RESULT 5
US-10-622-998-1
; Sequence 1, Application US/10622998
; Publication No. US20040105840A1
; GENERAL INFORMATION:
; APPLICANT: Kinstler, Olaf
; APPLICANT: Ladd, David
; APPLICANT: Papisov, Mikhail
; TITLE OF INVENTION: PROTEIN CONJUGATES WITH A WATER-SOLUBLE BIOCOMPATIBLE, BIODEGRAD
; TITLE OF INVENTION: POLYMER
; FILE REFERENCE: A-822
; CURRENT APPLICATION NUMBER: US/10/622,998
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 60/397,509
; PRIOR FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-622-998-1

Query Match      100.0%; Score 736; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.3e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

QY 61 YQILTMPSRNVQISNDLENLRLDLHLVLAFAFKSCHLPWASGLETLDSLGGLVLEASGYS 120
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Db 61 YQILTSMPNRNVIQISNDLENLRLDHLVAFSKSCHLPWASGLETLDSLGVLASGYS 120
121 TEVVALSRLOGLQDMLWQLDLSGPC 146
121 TEVVALSRLOGLQDMLWQLDLSGPC 146

RESULT 6
US-10-658-834A-211
; Sequence 211, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
; TITLE OF INVENTION: Acid
; TITLE OF INVENTION: Molecules and Related Applications
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 211
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank AAA60470
; DATABASE ENTRY DATE: 1995-01-13
US-10-658-834A-211

Query Match 100.0%; Score 736; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.3e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60
Db 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60
Qy 61 YQILTSMPNRNVIQISNDLENLRLDHLVAFSKSCHLPWASGLETLDSLGVLASGYS 120
Db 61 YQILTSMPNRNVIQISNDLENLRLDHLVAFSKSCHLPWASGLETLDSLGVLASGYS 120
Qy 121 TEVVALSRLOGLQDMLWQLDLSGPC 146
Db 121 TEVVALSRLOGLQDMLWQLDLSGPC 146

RESULT 8
US-10-872-198-127
; Sequence 127, Application US/10872198
; Publication No. US2005002897A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich HAUPTS
; APPLICANT: Andre KOLTERMANN
; APPLICANT: Andreas SCHEIDIG
; APPLICANT: Christian VOETSMER
; APPLICANT: Ulrich Kettling
; TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF
; FILE REFERENCE: 04156.0002U4
; CURRENT APPLICATION NUMBER: US/10/872,198
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,518
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 04003058
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 127
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-872-198-127

Query Match 100.0%; Score 736; DB 5; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.3e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 61 YQILTSMPNRNVIQISNDLENLRLDHLVAFSKSCHLPWASGLETLDSLGVLASGYS 120
121 TEVVALSRLOGLQDMLWQLDLSGPC 146
121 TEVVALSRLOGLQDMLWQLDLSGPC 146

RESULT 7
US-10-468-496-1
; Sequence 1, Application US/10468496
; Publication No. US20040180386A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
; TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-117
; CURRENT APPLICATION NUMBER: US/10/468,496
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19

Query Match 100.0%; Score 736; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.3e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60
Db 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60
Qy 61 YQILTSMPNRNVIQISNDLENLRLDHLVAFSKSCHLPWASGLETLDSLGVLASGYS 120
Db 61 YQILTSMPNRNVIQISNDLENLRLDHLVAFSKSCHLPWASGLETLDSLGVLASGYS 120
Qy 121 TEVVALSRLOGLQDMLWQLDLSGPC 146
Db 121 TEVVALSRLOGLQDMLWQLDLSGPC 146

RESULT 7
US-10-468-496-1
; Sequence 1, Application US/10468496
; Publication No. US20040180386A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
; TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-117
; CURRENT APPLICATION NUMBER: US/10/468,496
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19

Query Match 100.0%; Score 736; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.3e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	VPIQKVQDDTKLIIKTIIVTRIINDISHTQSVSSKQKVTGLDPIFGLHPILITLSKMDQTLLAV	60
Db	1	VPIQKVQDDTKLIIKTIIVTRIINDISHTQSVSSKQKVTGLDPIFGLHPILITLSKMDQTLLAV	60
QY	61	YQOILTSPMRNVIQISNDLENRLDLHLVLAFAFSKCHLPWASGLETLDLSGGVLEASGY	120
Db	61	YQOILTSPMRNVIQISNDLENRLDLHLVLAFAFSKCHLPWASGLETLDLSGGVLEASGY	120
QY	121	TEVVALSRLOQSLQDWLWOLDLSPGC	146
Db	121	TEVVALSRLOQSLQDWLWOLDLSPGC	146

RESULT 9
US-10-623-189-1
; Sequence 1, Application US/10623189
; Publication No. US2005020496A1
; GENERAL INFORMATION:
; APPLICANT: DEPROLI, Alex M.
; APPLICANT: ORAL, Elif Ariloglu
; APPLICANT: TAYLOR, Simeon I.
; APPLICANT: GARG, Abhimanyu
; TITLE OF INVENTION: USE OF LEPTIN FOR TREATING HUMAN LIPOATROPHY AND METHOD OF DETERM
; TITLE OF INVENTION: PREDISPOSITION TO SAID TREATMENT
; FILE REFERENCE: 54113.8005.US02
; CURRENT APPLICATION NUMBER: US/10/623,189
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 10/279,129
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: US 60/336,394
; PRIOR FILING DATE: 2001-10-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant Leptin Human 146 (rHu-Leptin 1-146)
US-10-623-189-1

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RESULT 10
US-10-502-344-22
; Sequence 22, Application US/10502344
; Publication No. US20050214762A1
; GENERAL INFORMATION:
; APPLICANT: ROSS, Richard
; APPLICANT: ARTYMIUK, Peter
; APPLICANT: SAYERS, Jon
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: 100042.55084US
; CURRENT APPLICATION NUMBER: US/10/502,344
; CURRENT FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: PCT/GB03/00253
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: GB 0201679.8

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RESULT 11
US-11-021-951-127
; Sequence 127, Application US/11021951
; Publication No. US20050175581A1
; GENERAL INFORMATION:
; APPLICANT: HAUPTS, Ulrich
; APPLICANT: KOLTERMANN, Andre
; APPLICANT: SCHEIDIG, Andreas
; APPLICANT: VOTSMEIER, Christian
; APPLICANT: Ketting, Ulrich
; APPLICANT: COCO, Wayne Michael
; TITLE OF INVENTION: New Biological Entities And The Pharmaceutical
; TITLE OF INVENTION: And Diagnostic Use Thereof
; FILE REFERENCE: 04156.0002U5
; CURRENT APPLICATION NUMBER: US/11/021,951
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: 10/872,198
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,518
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 04003058
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 127
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-951-127

US-09-804-409A-11

Query Match 100.0%; Score 736; DB 3; Length 167;
Best Local Similarity 100.0%; Pred. No. 5.le-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKITVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 22 VPIQKVDDTKTLIKITVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 81

QY 61 YQQILTSPSRNVIQISNDLENLRDLHLVLAFAKSKCHLPWASGLETLDSLGGLVLEASGYS 120
DB 82 YQQILTSPSRNVIQISNDLENLRDLHLVLAFAKSKCHLPWASGLETLDSLGGLVLEASGYS 141

QY 121 TEVVLSRQSGSLQDMLWQLDLSPGC 146
DB 142 TEVVLSRQSGSLQDMLWQLDLSPGC 167

Search completed: May 4, 2006, 22:02:16
Job time : 112.887 secs

TITLE OF INVENTION: Canine OB Protein Compositions and Methods

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: One Amgen Center Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: U.S.A.
ZIP: 91320

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/789,306
FILING DATE: 20-Feb-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/609,408
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Eggert, Joan D.
REFERENCE/DOCKET NUMBER: A-387

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 167 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Leader Sequence
LOCATION: -21 to -1
SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-789-306-3

Query Match 100.0%; Score 736; DB 3; Length 167;
Best Local Similarity 100.0%; Pred. No. 5.le-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKITVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 22 VPIQKVDDTKTLIKITVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 81

QY 61 YQQILTSPSRNVIQISNDLENLRDLHLVLAFAKSKCHLPWASGLETLDSLGGLVLEASGYS 120
DB 82 YQQILTSPSRNVIQISNDLENLRDLHLVLAFAKSKCHLPWASGLETLDSLGGLVLEASGYS 141

QY 121 TEVVLSRQSGSLQDMLWQLDLSPGC 146
DB 142 TEVVLSRQSGSLQDMLWQLDLSPGC 167

RESULT 15

US-09-804-409A-11

Sequence 11, Application US/09804409A
Patent No. US2002015100A1

GENERAL INFORMATION:
APPLICANT: KIEFFER, TIMOTHY J.
APPLICANT: CHEUNG, ANTHONY T.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATED PROTEIN
FILE REFERENCE: 029996/027 8721
CURRENT APPLICATION NUMBER: US/09/804,409A
CURRENT FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin ver. 2.1

SEQ ID NO 11
LENGTH: 167
TYPE: PRT
ORGANISM: Homo sapiens

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 4, 2006, 21:58:39 ; Search time 18.0619 Seconds
(without alignments)
374.135 Million cell updates/sec

Title: US-10-623-189-1
Perfect score: 736
Sequence: 1 VPIQKVQDDTKTLTKITVTR.....SRLOGLQDMLWOLDLSPGC 146

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Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA New:
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9: /SIDSS5/ptodata/2/pubpaa/US10_NEW_PUB.pep1.*
10: /SIDSS5/ptodata/2/pubpaa/US11_NEW_PUB.pep1.*
11: /SIDSS5/ptodata/2/pubpaa/US11_NEW_PUB.pep1.*
12: /SIDSS5/ptodata/2/pubpaa/US60_NEW_PUB.pep1.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	736	100.0	146	9	US-10-519-390-19
2	736	100.0	146	11	US-11-176-830-211
3	736	100.0	167	11	US-11-236-198-32
4	736	100.0	185	9	US-10-821-234-1384
5	736	100.0	397	11	US-11-192-219-47
6	734	99.7	146	11	US-11-176-830-666
7	734	99.7	146	11	US-11-176-830-672
8	734	99.7	146	11	US-11-176-830-677
9	734	99.7	146	11	US-11-176-830-683
10	733	99.6	146	11	US-11-176-830-665
11	733	99.6	146	11	US-11-176-830-671
12	733	99.6	146	11	US-11-176-830-673
13	733	99.6	146	11	US-11-176-830-676
14	733	99.6	146	11	US-11-176-830-682
15	733	99.6	146	11	US-11-236-198-36
16	731	99.3	146	11	US-11-176-830-674
17	731	99.3	146	11	US-11-176-830-675
18	731	99.3	146	11	US-11-176-830-679
19	731	99.3	146	11	US-11-176-830-681
20	730	99.2	146	11	US-11-176-830-678
21	730	99.2	146	11	US-11-176-830-680

ALIGNMENTS

RESULT 1

US-10-519-390-19
Sequence 19, Application US/10519390
Publication No. US20060008872A1

GENERAL INFORMATION:
APPLICANT: MEDEXGEN Inc.

APPLICANT: CHUNG, Yong-Hoon

APPLICANT: LEE, Hak-sup

APPLICANT: YI, Ki-Wan

APPLICANT: KIM, Jae-Youn

APPLICANT: HEO, Youn-Hwa

TITLE OF INVENTION: A method of improving efficacy of biological response-modifying

TITLE OF INVENTION: proteins and the example mutants

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/519,390

CURRENT FILING DATE: 2004-12-23

PRIOR APPLICATION NUMBER: KR10-2003-0051846

PRIOR FILING DATE: 2003-07-26

NUMBER OF SEQ ID NOS: 65

SOFTWARE: Kopatentin 1.71

SEQ ID NO 19

LENGTH: 146

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: LPT: 41st or 92nd Phe is replaced by Val.

US-10-519-390-19

Query Match 100.0%; Score 736; DB 9; Length 146;

Best Local Similarity 100.0%; Pred. No. 2.4e-65;

Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKTLTKITVTRINDISHTQSVSSKQKVTGLDIPGLHPIITLSKMDQTLAV 60

Db 1 VPIQKVQDDTKTLTKITVTRINDISHTQSVSSKQKVTGLDIPGLHPIITLSKMDQTLAV 60

Qy 61 YQQLTSMPSRNVQISNDLENLDLHLVAFSKSCHLPWASGLETLDLSGLGVLEASGYS 120

Db 61 YQQLTSMPSRNVQISNDLENLDLHLVAFSKSCHLPWASGLETLDLSGLGVLEASGYS 120

Qy 121 TEVVALSRLOGLQDMLWOLDLSPGC 146

Db 121 TEVVALSRLOGLQDMLWOLDLSPGC 146

Sequence 663, App
Sequence 664, App
Sequence 667, App
Sequence 668, App
Sequence 31, Appl
Sequence 5, Appl
Sequence 670, App
Sequence 669, App
Sequence 37, Appl
Sequence 33, Appl
Sequence 28, Appl
Sequence 39, Appl
Sequence 35, Appl
Sequence 34, Appl
Sequence 8, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 29, Appl
Sequence 30, Appl
Sequence 1, Appl
Sequence 2, Appl
Sequence 54, Appl

22 728 98.9 146 11 US-11-176-830-663
23 728 98.9 146 11 US-11-176-830-664
24 728 98.9 146 11 US-11-176-830-667
25 728 98.9 146 11 US-11-176-830-668
26 728 98.9 146 11 US-11-236-198-31
27 727 98.8 146 9 US-10-926-798-5
28 723 98.2 146 11 US-11-176-830-670
29 722 98.1 146 11 US-11-176-830-669
30 721 98.0 146 11 US-11-236-198-37
31 672 91.3 167 11 US-11-236-198-33
32 628 85.3 167 11 US-11-236-198-28
33 627 85.2 167 11 US-11-236-198-39
34 624 84.8 146 11 US-11-236-198-35
35 619 84.1 167 11 US-11-236-198-34
36 608 82.6 178 9 US-10-926-798-8
37 605 82.2 167 11 US-11-236-198-38
38 603 81.9 178 9 US-10-926-798-15
39 601 81.7 178 9 US-10-926-798-16
40 600 81.5 178 9 US-10-926-798-17
41 599 81.4 146 11 US-11-236-198-29
42 586.5 79.7 163 11 US-11-236-198-30
43 154 20.9 32 9 US-10-841-218-1
44 125 17.0 26 9 US-10-841-218-2
45 120 16.3 22 11 US-11-236-198-54

```
RESULT 2
US-11-176-830-211
; Sequence 211, Application US/11176830
; Publication No. US2006020116A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Dittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
; FILE REFERENCE: 17109-012002 (922B)
; CURRENT APPLICATION NUMBER: US/11/176,830
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: 10/658,834
; PRIOR FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 211
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank AAA60470
; DATABASE ENTRY DATE: 1995-01-13
US-11-176-830-211

Query Match 100.0%; Score 736; DB 11; Length 146;
Best Local Similarity 100.0%; Pred. No. 2.4e-65;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
QY 61 YQQLTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
DB 61 YQQLTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
QY 121 TEVVALSRQGSLOQMLWQDLSPGC 146
DB 121 TEVVALSRQGSLOQMLWQDLSPGC 146

RESULT 3
US-11-236-198-32
; Sequence 32, Application US/11236198
; Publication No. US2006030530A1
; GENERAL INFORMATION:
; APPLICANT: Yen, Frances
; APPLICANT: Erickson, Mary Ruth
; APPLICANT: Fruebis, Joachim
; APPLICANT: Bihain, Bernard
; TITLE OF INVENTION: Methods Of Screening For Compounds That Modulate the
; TITLE OF INVENTION: LSR-Leptin Interaction and Their Use in the Prevention
; TITLE OF INVENTION: and Treatment of Obesity-Related Diseases
; FILE REFERENCE: 70 US2,REG
; CURRENT APPLICATION NUMBER: US/11/236,198
; CURRENT FILING DATE: 2005-09-27
; PRIOR APPLICATION NUMBER: US/09/668,558
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,506
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: Patent.pm
; SEQ ID NO 32
; LENGTH: 167
; TYPE: PRT

Query Match 100.0%; Score 736; DB 11; Length 146;
Best Local Similarity 100.0%; Pred. No. 2.4e-65;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
QY 61 YQQLTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
DB 61 YQQLTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
QY 121 TEVVALSRQGSLOQMLWQDLSPGC 146
DB 121 TEVVALSRQGSLOQMLWQDLSPGC 146

RESULT 4
US-10-821-234-1384
; Sequence 1384, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1384
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1384

Query Match 100.0%; Score 736; DB 9; Length 185;
Best Local Similarity 100.0%; Pred. No. 3.2e-65;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 40 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 99
QY 61 YQQLTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
DB 100 YQQLTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 159
QY 121 TEVVALSRQGSLOQMLWQDLSPGC 146
DB 160 TEVVALSRQGSLOQMLWQDLSPGC 185

RESULT 5
US-11-192-219-47
; Sequence 47, Application US/11192219
; Publication No. US20050272656A1
; GENERAL INFORMATION:
; APPLICANT: Matthews, William
; TITLE OF INVENTION: USES FOR WSX LIGANDS
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
```

```
; ORGANISM: Homo sapiens
US-11-236-198-32

Query Match 100.0%; Score 736; DB 11; Length 167;
Best Local Similarity 100.0%; Pred. No. 2.8e-65;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 22 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 81
QY 61 YQQLTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
DB 82 YQQLTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 141
QY 121 TEVVALSRQGSLOQMLWQDLSPGC 146
DB 142 TEVVALSRQGSLOQMLWQDLSPGC 167
```

```
;
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/192,219
; FILING DATE: 27-Jul-2005
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,197
; FILING DATE: 20-Jun-1996
; APPLICATION NUMBER: 08/585005
; FILING DATE: 08-Jan-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: P-40,378
; REFERENCE/DOCKET NUMBER: P0986P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 397 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-11-192-219-47

Query Match 100.0%; Score 736; DB 11; Length 397;
Best Local Similarity 100.0%; Pred. No. 8.8e-65; Indels 0; Gaps 0;
Matches 146; Conservative 0; Mismatches 0;

Qy 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Db 22 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 81
Qy 61 YQQLTSMPSRNVIQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDLSLGGVLEASGY 120
Db 82 YQQLTSMPSRNVIQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDLSLGGVLEASGY 141
Qy 121 TEVVALSRLOGLQDMLWQLDLSFGC 146
Db 142 TEVVALSRLOGLQDMLWQLDLSFGC 167

RESULT 6
US-11-176-830-666
; Sequence 666, Application US/11/176830
; Publication No. US20060020116A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding N
; FILE REFERENCE: 17109-012002 (922B)
; CURRENT APPLICATION NUMBER: US/11/176,830
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: 10/658,834
; PRIOR FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 666
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-176-830-672
Query Match 99.7%; Score 734; DB 11; Length 146;
Best Local Similarity 99.3%; Pred. No. 3.7e-65;
Matches 145; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Db 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Qy 61 YQQLTSMPSRNVIQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDLSLGGVLEASGY 120
Db 61 YQQLTSMPSRNVIQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDLSLGGVLEASGY 120
Qy 121 TEVVALSRLOGLQDMLWQLDLSFGC 146
Db 121 TEVVALSRLOGLQDMLWQLDLSFGC 146

RESULT 7
US-11-176-830-672
; Sequence 672, Application US/11/176830
; Publication No. US20060020116A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding N
; FILE REFERENCE: 17109-012002 (922B)
; CURRENT APPLICATION NUMBER: US/11/176,830
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: 10/658,834
; PRIOR FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 672
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-176-830-677
Query Match 99.7%; Score 734; DB 11; Length 146;
Best Local Similarity 99.3%; Pred. No. 3.7e-65;
Matches 145; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Db 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Qy 61 YQQLTSMPSRNVIQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDLSLGGVLEASGY 120
Db 61 YQQLTSMPSRNVIQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDLSLGGVLEASGY 120
Qy 121 TEVVALSRLOGLQDMLWQLDLSFGC 146
Db 121 TEVVALSRLOGLQDMLWQLDLSFGC 146

RESULT 8
US-11-176-830-677
; Sequence 677, Application US/11/176830
; Publication No. US20060020116A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
```

```
;
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/192,219
; FILING DATE: 27-Jul-2005
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,197
; FILING DATE: 20-Jun-1996
; APPLICATION NUMBER: 08/585005
; FILING DATE: 08-Jan-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: P-40,378
; REFERENCE/DOCKET NUMBER: P0986P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 397 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-11-192-219-47

Query Match 100.0%; Score 736; DB 11; Length 397;
Best Local Similarity 100.0%; Pred. No. 8.8e-65; Indels 0; Gaps 0;
Matches 146; Conservative 0; Mismatches 0;

Qy 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Db 22 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 81
Qy 61 YQQLTSMPSRNVIQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDLSLGGVLEASGY 120
Db 82 YQQLTSMPSRNVIQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDLSLGGVLEASGY 141
Qy 121 TEVVALSRLOGLQDMLWQLDLSFGC 146
Db 142 TEVVALSRLOGLQDMLWQLDLSFGC 167

RESULT 6
US-11-176-830-666
; Sequence 666, Application US/11/176830
; Publication No. US20060020116A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding N
; FILE REFERENCE: 17109-012002 (922B)
; CURRENT APPLICATION NUMBER: US/11/176,830
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: 10/658,834
; PRIOR FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 666
; LENGTH: 146
```

; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
; FILE REFERENCE: 17109-012002 (922B)
; CURRENT APPLICATION NUMBER: US/11/176,830
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: 10/658,834
; PRIOR FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 677
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-176-830-677

Query Match 99.7%; Score 734; DB 11; Length 146;
Best Local Similarity 99.3%; Pred. No. 3.7e-65;
Matches 145; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
DB 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60

QY 61 YQILTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
DB 61 YQILTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120

QY 121 TEVVALSRLOGSLODMLWQLDLSPGC 146

DB 121 TEVVALSRLOGSLODMLWQLDLSPGC 146

RESULT 9
US-11-176-830-683
; Sequence 683, Application US/11/176830
; Publication No. US20060020116A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
; FILE REFERENCE: 17109-012002 (922B)
; CURRENT APPLICATION NUMBER: US/11/176,830
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: 10/658,834
; PRIOR FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 683
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-176-830-683

Query Match 99.7%; Score 734; DB 11; Length 146;
Best Local Similarity 99.3%; Pred. No. 3.7e-65;
Matches 145; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
DB 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60

QY 61 YQILTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
DB 61 YQILTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120

QY 121 TEVVALSRLOGSLODMLWQLDLSPGC 146
DB 121 TEVVALSRLOGSLODMLWQLDLSPGC 146

RESULT 10
US-11-176-830-665
; Sequence 665, Application US/11/176830
; Publication No. US20060020116A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding N
; FILE REFERENCE: 17109-012002 (922B)
; CURRENT APPLICATION NUMBER: US/11/176,830
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: 10/658,834
; PRIOR FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 665
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-176-830-665

Query Match 99.6%; Score 733; DB 11; Length 146;
Best Local Similarity 99.3%; Pred. No. 4.7e-65;
Matches 145; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
DB 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60

QY 61 YQILTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
DB 61 YQILTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120

QY 121 TEVVALSRLOGSLODMLWQLDLSPGC 146
DB 121 TEVVALSRLOGSLODMLWQLDLSPGC 146

RESULT 11
US-11-176-830-671
; Sequence 671, Application US/11/176830
; Publication No. US20060020116A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding N
; FILE REFERENCE: 17109-012002 (922B)
; CURRENT APPLICATION NUMBER: US/11/176,830
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: 10/658,834
; PRIOR FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21

Best Local Similarity 99.3%; Pred. No. 4.7e-65;
Matches 145; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
-Qy 1 VPIQKVDDTKTLIKITVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Db 1 VPIQKVDDTKTLIKITVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Qy 61 YQILTSMPSRNVIQISNDLENLRLDLHLVLAFAFKSCHLPWASGLETLDSLGGLVLEASGYS 120
Db 61 YQILTSMPSRNVIQISNDLENLRLDLHLVLAFAFKSCHLPWASGLETLDSLGGLVLEASGYS 120
Qy 121 TEVVALSRQGSIQDMLWQLDLSPGC 146
Db 121 TEVVALSRQGSIQDMLWQLDLSPGC 146

RESULT 15
US-11-236-198-36
; Sequence 36, Application US/11236198
; Publication No. US20060030530A1
; GENERAL INFORMATION:
; APPLICANT: Yen, Frances
; APPLICANT: Erickson, Mary Ruth
; APPLICANT: Fruebis, Joachim
; APPLICANT: Bihain, Bernard
; TITLE OF INVENTION: Methods Of Screening For Compounds That Modulate the
; TITLE OF INVENTION: LSR-Leptin Interaction and Their Use in the Prevention
; TITLE OF INVENTION: and Treatment of Obesity-Related Diseases
; FILE REFERENCE: 70.US2.REG
; CURRENT APPLICATION NUMBER: US/11/236,198
; CURRENT FILING DATE: 2005-09-27
; PRIOR APPLICATION NUMBER: US/09/668,558
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,506
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: Patent.pm
; SEQ ID NO 36
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Pan troglodytes
US-11-236-198-36

Query Match 99.6%; Score 733; DB 1; Length 146;
Best Local Similarity 99.3%; Pred. No. 4.7e-65;
Matches 145; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPIQKVDDTKTLIKITVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Db 1 VPIQKVDDTKTLIKITVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Qy 61 YQILTSMPSRNVIQISNDLENLRLDLHLVLAFAFKSCHLPWASGLETLDSLGGLVLEASGYS 120
Db 61 YQILTSMPSRNVIQISNDLENLRLDLHLVLAFAFKSCHLPWASGLETLDSLGGLVLEASGYS 120
Qy 121 TEVVALSRQGSIQDMLWQLDLSPGC 146
Db 121 TEVVALSRQGSIQDMLWQLDLSPGC 146

Search completed: May 4, 2006, 22:02:58
Job time : 19.0619 secs

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OM protein - protein search, using sw model

Run on: May 4, 2006, 21:46:23 ; Search time 137.526 Seconds
(without alignments)
463.258 Million cell updates/sec

Title: US-10-623-189-2

Perfect score: 731

Sequence: 1 VFPIQVQDDTKTLTIIVTR.....SRLOQLDMLQDLSPGC 145

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001s.*
- 5: Geneseq2002s.*
- 6: Geneseq2003as.*
- 7: Geneseq2003bs.*
- 8: Geneseq2004s.*
- 9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	731	100.0	145	2 AAW00302	Aaw00302 Human del
2	731	100.0	145	2 AAW00541	Aaw00541 Human mat
3	731	100.0	145	2 AAW30893	Aaw30893 Synthetic
4	731	100.0	145	3 AAY92815	Aay92815 Mature le
5	731	100.0	145	3 AAY83769	Aay83769 Human OB
6	731	100.0	145	3 AAY97889	Aay97889 Mutant ma
7	731	100.0	145	3 AAY95787	Aay95787 Mature re
8	731	100.0	145	3 AAB14266	Aab14266 Mature hu
9	731	100.0	145	6 ABR57163	Abr57163 Recombina
10	731	100.0	146	2 AAW34397	Aaw34397 Human Met
11	731	100.0	146	3 AAY97890	Aay97890 Mutant ma
12	731	100.0	146	3 AAY92262	Aay92262 Mature re
13	731	100.0	165	2 AAW00537	Aaw00537 Human obe
14	731	100.0	166	2 AAW00515	Aaw00515 Human obe
15	731	100.0	166	2 AAW00525	Aaw00525 Human obe
16	731	100.0	166	2 AAW00530	Aaw00530 Human obe
17	731	100.0	166	2 AAW00532	Aaw00532 Human obe
18	731	100.0	166	2 AAW00531	Aaw00531 Human obe
19	731	100.0	166	2 AAW00523	Aaw00523 Human obe
20	731	100.0	166	2 AAW00533	Aaw00533 Human obe
21	731	100.0	166	3 AAB28450	Aab28450 Human OB
22	731	100.0	166	3 AAY87728	Aay87728 Murine OB
23	731	100.0	166	3 AAB28469	Aab28469 Human OB
24	731	100.0	166	5 AABG74166	Aabg74166 Human obe

ALIGNMENTS

RESULT 1

AAW00302

ID AAW00302 standard; protein; 145 AA.

XX AC AAW00302;

XX DT 20-NOV-1996 (first entry)

XX DE Human delta Gln28 ob protein.

XX KW Human; obesity protein; ob; fat cell cDNA library; primer; PCR;
KW polymerase chain reaction; amplify; dipeptide leader; antibody;
KW peripheral adipose tissue; weight gain; obese; peptide hormone;
KW fat deposit; type II diabetes; cardiovascular disease; cancer.

XX OS Homo sapiens.

XX PN MO9624670-AI.

XX PD 15-AUG-1996.

XX PF 29-JAN-1996; 96WO-US001411.

XX PR 06-FEB-1995; 95US-00384493.

XX PR 26-MAY-1995; 95US-00451250.

XX PA (ELIL) LILLY & CO ELI.

XX PI Basinski MB, Schoner BE;

XX DR WPI; 1996-384442/38.

XX DR N-PSDB; AAT40259, AAT40260.

XX PT New DNA encoding two forms of the human obesity gene product - and related vectors and transformed cells, used to produce recombinant proteins for treating obesity.

XX PS Claim 4; Page 23; 30pp; English.

XX CC The sequences given in AAW00301-02 represent two forms of the human obesity protein, ob, in which Ala27Gln28 in AAW00301 are replaced by a single Thr in AAW00302. The nucleic acid sequences were isolated from a human fat cell cDNA library using the primer sequences given in AAT40261-64. The ob proteins are pref. expressed with a dipeptide leader sequence of Met-Arg or Met-Tyr. Experiments have suggested that the ob proteins are released by peripheral adipose tissue and are capable of controlling weight gain in normal and obese mice. The ob proteins are thought to be

Abb84118 Truncated
Abu64563 Human ob
Adt93139 Human ob
Abb84141 Truncated
Abb84140 Truncated
Abb84139 Truncated
Aaw34396 Human Met
Aaw00013 Acid stab
Aar99490 Chimeric
Aaw00539 Human mat
Aaw30892 Synthetic
Aaw34482 Human obe
Aaw08595 Properly
Aaw28896 Biologica
Aaw08599 Properly
Aaw10151 Properly
Aaw22900 Biologica
Aaw22901 Biologica
Aaw30791 Obesity p
Aaw26191 Obesity p
Aaw26194 Obesity p

CC circulating peptide hormones which regulate the size of a bodies fat
CC deposits. They can be used to treat obesity and to reduce the risk of
CC type II diabetes, cardiovascular disease and cancer. Anti-ob protein
CC antibodies may be used for diagnostic purposes
XX
SQ Sequence 145 AA;
Query Match 100.0%; Score 731; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.8e-72;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPIQKVDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLKMDQTLAVY 60
DB 1 VPIQKVDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLKMDQTLAVY 60
QY 61 QQILTSMPSRNVIQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGGLVLEASGYST 120
DB 61 QQILTSMPSRNVIQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGGLVLEASGYST 120
QY 121 EVVALSRLOGLQDMLWQLDLSFGC 145
DB 121 EVVALSRLOGLQDMLWQLDLSFGC 145
RESULT 2
AAW00541
ID AAW00541 standard; protein; 145 AA.
XX
AC AAW00541;
XX
DT 13-SEP-1996 (first entry)
XX
DE Human mature obesity protein variant.
XX
KW Obesity; mouse; OBP; leptin; hormone; body weight regulation; diabetes;
KW food intake; energy expenditure; high blood pressure; cholesterol; human;
KW gene therapy; antibody; cancer; Kobe beef; Foie gras; immunoassay.
XX
OS Homo sapiens.
XX
PN GB2292382-A.
XX
PD 21-FEB-1996.
XX
PF 17-AUG-1995; 95GB-00016947.
XX
PR 17-AUG-1994; 94US-00292345.
PR 30-NOV-1994; 94US-00347563.
PR 10-MAY-1995; 95US-00438431.
PR 07-JUN-1995; 95US-00483211.
XX
PA (UYRQ) UNIV ROCKEFELLER.
XX
PI Friedman JM, Zhang Y, Proenca R, Maffei M, Halasa JL, Gajiwala K;
PI Burley SK;
XX
DR WPI; 1996-099009/11.
XX
PT Obesity polypeptide(s) able to modulate body wt. - useful for e.g.
PT reducing wt. in treatment of diabetes, high blood pressure and high
PT cholesterol and for cosmetic reasons.
XX
PS Claim 11; Page ?; 304pp; English.
XX
CC AAW00538-W00541 represent the mature proteins of the murine and human
CC obesity polypeptides (OBP) (full length sequences represented by AAR92719
CC and AAR92720). OBP (also known as leptin) is a hormone involved in the
CC regulation of body weight. This sequence has effects on both food intake
CC and energy expenditure. OBP and its analogues are useful for modifying
CC body weight (optionally combined with known medicaments), for treating
CC diabetes, high blood pressure or high cholesterol. The DNA encoding this
CC sequence (and sequences complementary to it) can be used in gene therapy
CC for modifying body weight. This protein can be used for reducing weight

CC for health or cosmetic reasons in obese humans, or to produce leaner food
CC animals. Antagonists of OBP (including antibodies) are useful for
CC increasing body weight, e.g. for treating weight loss associated with
CC cancer, or for cosmetic reasons in humans, or for production of Kobe beef
CC or Foie gras in domestic animals. OBP antibodies (Ab) can also be used in
CC diagnostic immunoassays for the presence of OBP. The formation of Ab-OBP
CC complexes enables in vitro evaluation of levels of OBP in a sample,
CC especially to detect diseases associated with elevated or decreased
CC levels, and to monitor treatment of these diseases
XX
SQ Sequence 145 AA;
Query Match 100.0%; Score 731; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.8e-72;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPIQKVDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLKMDQTLAVY 60
DB 1 VPIQKVDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLKMDQTLAVY 60
QY 61 QQILTSMPSRNVIQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGGLVLEASGYST 120
DB 61 QQILTSMPSRNVIQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGGLVLEASGYST 120
QY 121 EVVALSRLOGLQDMLWQLDLSFGC 145
DB 121 EVVALSRLOGLQDMLWQLDLSFGC 145
RESULT 3
AAW30893
ID AAW30893 standard; protein; 145 AA.
XX
AC AAW30893;
XX
DT 20-APR-1998 (first entry)
XX
DE Synthetic obesity protein.
XX
KW Obesity protein; sucrose; trehalose; treatment; obesity; diabetes;
KW cardiovascular disease; cancer.
XX
OS Synthetic.
XX
PN EP9797999-A2.
XX
PD 01-OCT-1997.
XX
PF 24-MAR-1997; 97EP-00301995.
XX
PR 26-MAR-1996; 96US-0014177P.
PR 05-APR-1996; 96US-0014951P.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Beals JM, Edwards MJ, Pikal MJ, Rinella JV;
XX
DR WPI; 1997-472913/44.
XX
PT Pharmaceutical compositions comprising obesity protein - and sucrose
PT and/or trehalose.
XX
PS Claim 3; Page 44-45; 48pp; English.
XX
CC A novel pharmaceutical composition comprises an obesity protein, e.g. the
CC present sequence, together with sucrose and/or trehalose. The composition
CC can be used to treat obesity and associated disorders, e.g. diabetes,
CC cardiovascular disease and cancer. The composition is stable and easy to
CC manufacture
XX
SQ Sequence 145 AA;
Query Match 100.0%; Score 731; DB 2; Length 145;

Best Local Similarity 100.0%; Pred. No. 1.8e-72;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVDDTKTLTKTIIVTRINDISHTSVSSKQKVTGLDFPGHLPILTLKMDQTLAVY 60
Db 1 VPIQKVDDTKTLTKTIIVTRINDISHTSVSSKQKVTGLDFPGHLPILTLKMDQTLAVY 60
Qy 61 QQILTSMPNRNVIQISNDLENLRDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYST 120
Db 61 QQILTSMPNRNVIQISNDLENLRDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYST 120
Qy 121 EVVALSRQLQSLQDMLWQLDLSGPC 145
Db 121 EVVALSRQLQSLQDMLWQLDLSGPC 145

RESULT 4
AAY92815
ID AAY92815 standard; protein; 145 AA.

AC AC
XX AAY92815;
DT 29-AUG-2000 (first entry)

XX Mature leptin receptor agonist analogue.

XX Leptin; analogue; lean body mass; receptor; ligand; agonist; inhibitor;
KW anorexia; malnutrition; cachexia; animal husbandry; immunomodulator;
KW catabolic.

OS Homo sapiens.
OS Synthetic.

XX Key Location/Qualifiers

FT Key
FT Misc-difference 4 /note= "can be replaced with Glu"
FT Misc-difference 7 /note= "can be replaced with Glu"
FT Misc-difference 22 /note= "can be replaced with Glu"
FT Misc-difference 27 /note= "can be replaced with Gln or Asp"
FT Misc-difference 27 /note= "can be replaced with Ala"
FT Misc-difference 33 /note= "can be replaced with Glu"
FT Misc-difference 53 /note= "can be replaced with Glu"
FT Misc-difference 53 /note= "can be replaced with methionine sulfoxide, Leu,
FT Ile, Val, Ala or Gly"
FT Misc-difference 55 /note= "can be replaced with Glu"
FT Misc-difference 61 /note= "can be replaced with Glu"
FT Misc-difference 62 /note= "can be replaced with Glu"
FT Misc-difference 67 /note= "can be replaced with Glu"
FT Misc-difference 67 /note= "can be replaced with methionine sulfoxide, Leu,
FT Ile, Val, Ala or Gly"
FT Misc-difference 71 /note= "can be replaced with Gln, Glu or Asp"
FT Misc-difference 74 /note= "can be replaced with Glu"
FT Misc-difference 76 /note= "can be replaced with Ala"
FT Misc-difference 77 /note= "can be replaced with Gln or Asp"
FT Misc-difference 81 /note= "can be replaced with Gln or Asp"
FT Misc-difference 96 /note= "can be replaced with Gln, Asn, Ala, Gly, Ser or
FT Pro"
FT Misc-difference 99 /note= "can be replaced with Ala, Glu, Asp, Asn, Met,
FT Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val or Leu"
FT Misc-difference 100

FT /note= "can be replaced with Ser, Asn, Gly, His, Pro, Thr
FT or Val"
FT Misc-difference 101 /note= "can be replaced with Arg"
FT Misc-difference 102 /note= "can be replaced with Ala"
FT Misc-difference 104 /note= "can be replaced with Gln"
FT Misc-difference 105 /note= "can be replaced with Lys or Ser"
FT Misc-difference 106 /note= "can be replaced with Pro"
FT Misc-difference 107 /note= "can be replaced with Glu"
FT Misc-difference 110 /note= "can be replaced with Asp"
FT Misc-difference 117 /note= "can be replaced with Leu"
FT Misc-difference 129 /note= "can be replaced with Glu"
FT Misc-difference 133 /note= "can be replaced with Glu"
FT Misc-difference 135 /note= "can be replaced with methionine sulfoxide, Leu,
FT Ile, Val, Ala or Gly"
FT Misc-difference 137 /note= "can be replaced with Ala, Glu, Asp, Asn, Met,
FT Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val or Leu"
FT Misc-difference 138 /note= "can be replaced with Glu"
FT XX
FT PN
FT WO200024418-A1.
XX PD
XX 04-MAY-2000.
XX 27-OCT-1999; 99WO-US025120.
XX 27-OCT-1998; 98US-00179461.
XX (ELIL) LILLY & CO ELI.
XX Heiman ML, Tinsley FC, Caro JP;
XX WPI; 2000-350589/30.
XX Method for preventing the loss of lean tissue mass useful in therapy
FT during catabolic states such as cachexia resulting from illnesses such as
FT anorexia and malnutrition.
XX Claim 4; Page 16; 43pp; English.
XX Leptin analogues comprise this sequence having at least one substitution
CC as featured above. A glutamine residue may be present at position 28 (see
CC AA92712) or absent as in this sequence. A claimed method for preventing
CC the loss of lean tissue mass associated with improper nutrition comprises
CC administering to a mammal a leptin receptor agonist, such as the present
CC ligand is preferably a human leptin receptor agonist, such as the present
CC sequence. Binding of the leptin receptor inhibitor leads to an increase
CC of leptin production and a consequent increase in body mass. The method
CC can be used for therapy in catabolic states such as cachexia resulting
CC from illnesses such as anorexia and malnutrition. Methods of increasing
CC lean tissue growth are also useful in the fields of veterinary science
CC and animal husbandry in benefiting the health and quality of livestock
XX Sequence 145 AA;
SQ

Query Match 100.0%; Score 731; DB 3; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.8e-72;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVDDTKTLTKTIIVTRINDISHTSVSSKQKVTGLDFPGHLPILTLKMDQTLAVY 60
Db 1 VPIQKVDDTKTLTKTIIVTRINDISHTSVSSKQKVTGLDFPGHLPILTLKMDQTLAVY 60

QY 61 QQILTSMPSSRNVIQISNDLENRLDLHLVLAFAFSKSLPWSAGLETLDLSLGGVLEASGYST 120
 Db 61 QQILTSMPSSRNVIQISNDLENRLDLHLVLAFAFSKSLPWSAGLETLDLSLGGVLEASGYST 120
 QY 121 EVVALSRLQSLQDMLWQLDLSPGC 145
 Db 121 EVVALSRLQSLQDMLWQLDLSPGC 145

RESULT 5
 AAY83769
 ID AAY83769 standard; protein; 145 AA.
 XX
 AC AAY83769;
 XX
 DT 21-JUN-2000 (first entry)
 XX
 DE Human OB mutein (Val22-Cys167-delta(Gln49)).
 XX
 KW Antidiabetic; anorectic; antilipemic; dextran-leptin conjugate; human;
 mature OB protein; weight modulation; diabetes; blood lipid reduction;
 hyperlipidemia; lean body mass; insulin sensitivity; heart surgery;
 liposuction; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200009165-A1.
 XX
 PD 24-FEB-2000.
 XX
 PF 10-AUG-1999; 99WO-US018129.
 XX
 PR 10-AUG-1998; 98US-0096194P.
 PR 09-AUG-1999; 99US-00370684.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Litzinger DC;
 XX
 DR WPI; 2000-224187/19.
 XX
 PT New dextran-like conjugate compositions having improved efficacy and
 PT circulation time, increased solubility, and reduction in injection site
 PT reactions compared to native human leptin.
 XX
 PS Claim 8; Page; 52pp; English.
 XX
 CC The invention relates to a novel dextran-leptin conjugate comprising at
 CC least one low molecular dextran moiety, of 1-20 kDa, attached to at least
 CC one leptin moiety. The leptin moiety is preferably the mature human OB
 CC protein (AAY83768). That sequence corresponds to amino acids Val(22) to
 CC Cys(167) of the human OB protein. Alternatively the leptin may be a
 CC homologue of the human OB protein. This sequence corresponds to the
 CC Val(22)-Cys167 with the Gln49 (position 28 of AAY83768) deleted. The
 CC dextran-leptin conjugates can be used for weight modulation, treatment or
 CC prevention of diabetes, especially Type II, blood lipid reduction, e.g.
 CC hyperlipidemia, increasing lean body mass and increasing insulin
 CC sensitivity. The conjugates may also be used in combination therapies,
 CC e.g. prior to heart surgery or liposuction. The dextran-leptin conjugates
 CC have improved efficacy, longer plasma circulation time, and no kidney
 CC vacuole formation. They also have improved solubility and minimal
 CC injection site reactions. (Note: this sequence is not given in the
 CC specification but is generated from information given by the inventors)
 XX
 SQ Sequence 145 AA;

Query Match 100.0%; Score 731; DB 3; Length 145;
 Best Local Similarity 100.0%; Pred. No. 1.8e-72;
 Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKQDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLKMDQTLAVY 60

Db 1 VPIQKQDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLKMDQTLAVY 60
 QY 61 QQILTSMPSSRNVIQISNDLENRLDLHLVLAFAFSKSLPWSAGLETLDLSLGGVLEASGYST 120
 Db 61 QQILTSMPSSRNVIQISNDLENRLDLHLVLAFAFSKSLPWSAGLETLDLSLGGVLEASGYST 120
 QY 121 EVVALSRLQSLQDMLWQLDLSPGC 145
 Db 121 EVVALSRLQSLQDMLWQLDLSPGC 145

RESULT 6
 AAY97889
 ID AAY97889 standard; protein; 145 AA.
 XX
 AC AAY97889;
 XX
 DT 29-AUG-2000 (first entry)
 XX
 DE Mutant mature human leptin, delta-Q28.
 XX
 KW Leptin analogue; human; polyethylene glycol; site-specific PEGylation;
 obesity; anorectic; type II diabetes; antidiabetic; hyperlipidaemia;
 antilipaeamic; mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO2000021574-A2.
 XX
 PD 20-APR-2000.
 XX
 PF 13-OCT-1999; 99WO-US024401.
 XX
 PR 14-OCT-1998; 98US-00172644.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Gegg C, Kinastler O;
 XX
 DR WPI; 2000-329085/28.
 XX
 PT New dualPEGylated-leptin bioconjugate useful for treating obesity and
 PT diabetes has polyethylene glycol conjugated to two specific sites on the
 PT leptin molecule.
 XX
 PS Claim 2; Page; 55pp; English.
 XX
 CC The invention relates to a dual-PEGylated leptin bioconjugate comprising
 CC two polyethylene glycol (PEG) moieties attached site-specifically at two
 CC locations in a leptin protein. The invention also provides a site-
 CC directed poly-PEGylation strategy for proteins which results in
 CC homogenous preparations, and can be used with other biologically active
 CC agents including a variety of growth factors and peptide hormones. In
 CC leptin, a serine to cysteine substitution was engineered into the protein
 CC at position 77 (relative to the wild-type mature sequence AAY97871), and
 CC the S77C leptin analogue was PEGylated at the engineered Cys residue and
 CC at the N-terminus. Leptin is a protein which has been shown to cause
 CC weight loss in animals, indicating that it will be useful for causing
 CC weight loss in humans. However, these studies also indicate that leptin
 CC would need to be administered chronically and in a high concentration
 CC formulation to effectively treat obesity in humans. Leptin is insoluble
 CC at physiologic pH at relatively high concentrations, and when injected
 CC into an individual, forms precipitates at the injection site, which
 CC triggers an inflammatory response. The leptin bioconjugate of the
 CC invention provides leptin in a form which allows high dosage without the
 CC problems of leptin precipitates and associated inflammatory response at
 CC the injection site, as seen with prior art leptin compositions. The dual-
 CC PEGylated leptin molecule is large enough to avoid glomerular filtration
 CC and hence kidney vacuolation as seen with a single 20 kDa PEG conjugated
 CC leptin. The dual-PEGylated leptin conjugates are used to effect weight
 CC loss, and may also be used to treat type II diabetes and hyperlipidaemia.

CC Sequences AAY97889-Y97893 represent specifically claimed human mature
CC leptin analogues which may be dually-Pegylated according to the
CC invention. Note: The present sequence is not shown in the specification,
CC but is derived from the mature human leptin sequence given on page 12
XX
XX
SQ Sequence 145 AA;

Query Match 100.0%; Score 731; DB 3; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.8e-72;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPIQKVDDTKTLIKTIIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAVY 60
Db 1 VPIQKVDDTKTLIKTIIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAVY 60
Qy 61 QQILTSMPNRNVIQISNDLENRLDLHLVLAFAFSKCHLPWASGLETLDSLGVLASGYST 120
Db 61 QQILTSMPNRNVIQISNDLENRLDLHLVLAFAFSKCHLPWASGLETLDSLGVLASGYST 120
Qy 121 EVVALSRLOGLQDMLWQLDLSFGC 145
Db 121 EVVALSRLOGLQDMLWQLDLSFGC 145

RESULT 7
AAY95787
ID AAY95787 standard; protein; 145 AA.
XX
AC AAY95787;
DT 07-NOV-2000 (first entry)
XX
XX Mature recombinant human leptin rHu-Leptin 1-145.
DE
XX Leptin; rHu-Leptin 1-145; human; glycosylation; obesity; diabetes;
KW hyperlipidemia; antiobesity; antidiabetic; hyperlipemic; therapy.
KW
XX Homo sapiens.
OS
XX WO200047741-A1.
FN
XX 17-AUG-2000.
PD
XX 11-FEB-2000; 2000WO-US003652.
PF
XX 12-FEB-1999; 99US-00249675.
PR
XX (AMGE-) AMGEN INC.
PA
XX Martin FH, Elliott SG;
XX
XX WPI; 2000-524540/47.
DR

XX Glycosylated leptin proteins having a Stokes' radius greater than that of
XX a naturally occurring glycosylated human leptin useful for treating
XX obesity, diabetes and the effects of high blood lipid content.
XX
XX Claim 5; Page 31; 156pp; English.

XX The present sequence is that of mature recombinant human leptin, rHu-
XX Leptin 1-145. This is a natural variant of human leptin 1-146 (see
XX AAY95786) in which residue Gln-28 is absent. The invention is directed to
XX glycosylated leptin proteins that have a Stokes' radius greater than that
XX of naturally occurring human leptin. Preferred glycosylated leptins have
XX 1 or more sequence alterations to the present sequence to provide
XX glycosylation sites at amino acid positions 4, 8, 23, 43, 46, 47, 68, 69,
XX 91, 92, 96, 99, 100, 101, 102, 117 and 140, especially 46 + 68, 47 + 68,
XX 68 + 100, 68 + 101, 68 + 102, 68 + 117 and 99 + 101, or 2 + 46 + 68, 23 +
XX 46 + 68, 46 + 68 + 99, 46 + 68 + 101, 47 + 68 + 101, 47 + 68 + 117, 68 +
XX 101 + 117 and 66 + 102 + 117, or 2 + 46 + 68 + 91, 2 + 46 + 68 + 101, 23
XX + 46 + 68 + 91, 23 + 46 + 68 + 101 and 46 + 68 + 99 + 100, or 2 + 23 + 46
XX + 68 + 91, 2 + 46 + 68 + 91 + 101 and 23 + 46 + 68 + 91 + 101 (see
XX AAY95799-804). Nucleic acids encoding glycosylated leptins are provided,

CC as well as vectors and prokaryotic (especially bacterial) or eukaryotic
CC (especially human, monkey, BHK and CHO) host cells useful for recombinant
CC production of the glycosylated leptins. The glycosylated leptins, or
CC nucleic acids encoding them, are used in the treatment of obesity,
CC diabetes and the effects of high blood lipid content (claimed). They have
CC longer systemic circulation times in vivo than native leptins
XX
XX
SQ Sequence 145 AA;

Query Match 100.0%; Score 731; DB 3; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.8e-72;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPIQKVDDTKTLIKTIIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAVY 60
Db 1 VPIQKVDDTKTLIKTIIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAVY 60
Qy 61 QQILTSMPNRNVIQISNDLENRLDLHLVLAFAFSKCHLPWASGLETLDSLGVLASGYST 120
Db 61 QQILTSMPNRNVIQISNDLENRLDLHLVLAFAFSKCHLPWASGLETLDSLGVLASGYST 120
Qy 121 EVVALSRLOGLQDMLWQLDLSFGC 145
Db 121 EVVALSRLOGLQDMLWQLDLSFGC 145

RESULT 8
AAB14266
ID AAB14266 standard; protein; 145 AA.
XX
AC AAB14266;
DT 23-NOV-2000 (first entry)
XX
XX Mature human leptin #2.
DE
XX Human; leptin; OB protein; obesity; biodegradable; pH;
KW thermosensitive hydrogel; protein delivery.
KW
XX Homo sapiens.
OS
XX WO200038651-A1.
FN
XX 06-JUL-2000.
PD
XX 10-DEC-1999; 99WO-US029401.
PF
XX 23-DEC-1998; 98US-00221181.
PR
XX (AMGE-) AMGEN INC.
PA
XX Shah S, Dai W;
XX
XX WPI; 2000-482592/42.
DR
XX Pharmaceutical composition for sustained delivery of biologically active
XX agent, comprises biodegradable pH/thermosensitive polymetric matrix
XX containing the biologically active agent.
XX
XX Disclosure; Page; 51pp; English.
XX
XX The present invention relates to the use of biodegradable,
XX pH/thermosensitive hydrogels, which can be used to deliver biologically
XX active agents. The present sequence is a mature human leptin protein.
XX Leptin is also known as obesity protein (OB protein). This protein may be
XX used as the biologically active agent for use in the present invention.
XX Note: this sequence is not shown in the specification, but is derived
XX from information given by the inventors about SEQ ID 1 (AAB14265)
XX
XX Sequence 145 AA;
Query Match 100.0%; Score 731; DB 3; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.8e-72;

at physiologic pH at relatively high concentrations, and when injected into an individual, forms precipitates at the injection site, which triggers an inflammatory response. The leptin bioconjugate of the invention provides leptin in a form which allows high dosage without the problems of leptin precipitates and associated inflammatory response at the injection site, as seen with prior art leptin compositions. The dual-PEGylated leptin molecule is large enough to avoid glomerular filtration and hence kidney vacuolation as seen with a single 20 kDa PEG conjugated leptin. The dual-PEGylated leptin conjugates are used to effect weight loss, and may also be used to treat type II diabetes and hyperlipidaemia. Sequences AAY97889-Y97893 represent specifically claimed human mature leptin analogues which may be dually-PEGylated according to the invention. Note: The present sequence is not shown in the specification, but is derived from the mature human leptin sequence given on page 12

XX Sequence 146 AA;

Query Match 100.0%; Score 731; DB 3; Length 146;
Best Local Similarity 100.0%; Pred. No. 1.8e-72;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLKMDQTLAVY 60
Db |||||
2 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLKMDQTLAVY 61
QY 61 QQILTSMPSRNVIQISNDLENRLDLHLVLAFAFSKCHLPWASGLETLDSLGGVLEASGYST 120
Db |||||
62 QQILTSMPSRNVIQISNDLENRLDLHLVLAFAFSKCHLPWASGLETLDSLGGVLEASGYST 121
QY 121 EVVALSRLOGLQDMLWQLDLSFGC 145
Db |||||
122 EVVALSRLOGLQDMLWQLDLSFGC 146

RESULT 12

AAAY92262
ID AAY92262 standard; protein; 146 AA.

AC AAY92262;

XX 10-AUG-2000 (first entry)

DE Mature recombinant methionyl human leptin, rHu-leptin 1-145.

XX rHu-leptin 1-145; recombinant; mature protein; human leptin;

KW predisposition; screening; obesity.

KW Homo sapiens.

OS

FH Key Location/Qualifiers

FT Protein 2..145

FT /label= mature_protein

XX WO200020872-A1.

XX 13-APR-2000.

XX 21-SEP-1999; 99WO-US021903.

XX 02-OCT-1998; 98US-00165453.

PR 27-OCT-1998; 98US-00181836.

XX (AMGE-) AMGEN INC.

XX Mccamish MA, Hunt P, Lubina JA;

XX WPI; 2000-339110/29.

XX Novel method for determining a predisposition to successful leptin treatment of obesity by measuring baseline serum leptin levels.

XX Disclosure; Page; 40pp; English.

XX

CC This is the mature, recombinant methionyl human leptin, designated rHu-leptin 1-145, which is a variant of rHu-leptin 1-146 (see AAY92261). When compared with rHu-leptin 1-146, this sequence has a glutamine absent at position 28. The claimed method for determining the predisposition of an obese individual to respond to leptin, leptin analog or derivative treatment comprises determining a leptin level in the individual prior to treatment, and ascertaining if the leptin level is in the bottom 25 or 33 percent of leptin levels of obese individuals. The rHu-Leptin 1-146 or 1-145 (see AAY92262) or other analogues (e.g. AAY92263-66) may be used in treatment. The method can be used as a screening tool to determine the likelihood that an obese individual (i.e. an individual with a body mass index of greater than 27) not having co-morbidities of obesity, such as diabetes, dislipidaemias and hypertension, will respond to leptin administration with weight loss. Leptin is used for weight modulation (especially weight reduction), treatment of diabetes, blood lipid reduction, increasing lean body mass, and increasing insulin sensitivity, as well as the treatment of conditions associated with fertility, wound healing, hematopoietic conditions, angiogenic conditions and chronic stress conditions. Prescreening an individual's predisposition to respond to leptin administration may save on unnecessary treatments. Note: The specification provides the sequence of the mature protein which appears on pages 12-13, a methionyl residue is added at position 1 to create this rHu-Leptin 1-145 as described in the specification

XX Sequence 146 AA;

Query Match 100.0%; Score 731; DB 3; Length 146;
Best Local Similarity 100.0%; Pred. No. 1.8e-72;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLKMDQTLAVY 60
Db |||||
2 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLKMDQTLAVY 61
QY 61 QQILTSMPSRNVIQISNDLENRLDLHLVLAFAFSKCHLPWASGLETLDSLGGVLEASGYST 120
Db |||||
62 QQILTSMPSRNVIQISNDLENRLDLHLVLAFAFSKCHLPWASGLETLDSLGGVLEASGYST 121
QY 121 EVVALSRLOGLQDMLWQLDLSFGC 145
Db |||||
122 EVVALSRLOGLQDMLWQLDLSFGC 146

RESULT 13

AAW00537
ID AAW00537 standard; protein; 165 AA.

XX AAW00537;

XX 13-SEP-1996 (first entry)

XX Human obesity protein variant #15.

XX Obesity; mouse; OBP; leptin; hormone; body weight regulation; diabetes; food intake; energy expenditure; high blood pressure; cholesterol; human; gene therapy; antibody; cancer; Kobe beef; Foie gras; immunoassay.

OS Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..21

FT /note= "signal peptide"

FT Misc-difference 18

FT /note= "Y18G mutation"

FT Misc-difference 19

FT /note= "V19S mutation"

FT Misc-difference 20

FT /note= "Q20P mutation"

FT Misc-difference 21

FT /note= "delta A21 mutation"

FT Protein 22..165

XX /note= "obesity protein"

XX

Db 142 EVVALSRLOGLQDMLWQLDLSGPC 166

RESULT 15

AAW00525
ID AAW00525 standard; protein; 166 AA.

XX AC AAW00525;

XX DT 13-SEP-1996 (first entry)

XX DE Human obesity protein variant #5.

XX KW Obesity; mouse; OBP; leptin; hormone; body weight regulation; diabetes;
KW food intake; energy expenditure; high blood pressure; cholesterol; human;
KW gene therapy; antibody; cancer; Kobe beef; Foie gras; immunoassay.

XX OS Synthetic.

XX PH Key Location/Qualifiers
FT Peptide 1..21 /note= "signal peptide"
FT Misc-difference 2 /note= "H2G mutation"
FT Misc-difference 3 /note= "W3S mutation"
FT Misc-difference 4 /note= "G4S mutation"
FT Misc-difference 5 /note= "TSH mutation"
FT Misc-difference 6 /note= "L6H mutation"
FT Misc-difference 7 /note= "C7H mutation"
FT Misc-difference 8 /note= "G8H mutation"
FT Misc-difference 9 /note= "F9H mutation"
FT Misc-difference 10 /note= "L10H mutation"
FT Misc-difference 11 /note= "W11S mutation"
FT Misc-difference 12 /note= "L12S mutation"
FT Misc-difference 13 /note= "W13G mutation"
FT Misc-difference 14 /note= "P14L mutation"
FT Misc-difference 15 /note= "Y15V mutation"
FT Misc-difference 16 /note= "L16P mutation"
FT Misc-difference 17 /note= "F17R mutation"
FT Misc-difference 18 /note= "Y18G mutation"
FT Misc-difference 19 /note= "V19S mutation"
FT Misc-difference 20 /note= "Q20H mutation"
FT Misc-difference 21 /note= "A21M mutation"
FT Protein 22..166 /note= "obesity protein"

XX GB2292382-A.

XX PD 21-FEB-1996.

XX PF 17-AUG-1995; 95GB-00016947.

XX PR 17-AUG-1994; 94US-00292345.

XX PR 30-NOV-1994; 94US-00347563.

PR 10-MAY-1995; 95US-00438431.
PR 07-JUN-1995; 95US-00483211.
XX
XX PA (UYRQ) UNIV ROCKEFELLER.
XX
XX PI Friedman JM, Zhang Y, Proenca R, Maffei M, Halaas JL, Gajiwala K;
XX PI Burley SK;
XX DR WPI; 1996-099009/11.

XX OB Obesity polypeptide(s) able to modulate body wt. - useful for e.g.
FT reducing wt. in treatment of diabetes, high blood pressure and high
FT cholesterol and for cosmetic reasons.

XX PS Claim 11; Page ?; 304pp; English.

XX CC AAR92725-R92730, and AAW00516-W00537 represent variants of the murine and
CC human obesity polypeptides (OBP). This sequence has the signal peptide
CC region (residues 1-21) mutated in comparison to the wild type sequences
CC (represented by AAR92719 and AAR92720). OBP (also known as leptin) is a
CC hormone involved in the regulation of body weight. This sequence has
CC effects on both food intake and energy expenditure. OBP and its analogues
CC are useful for modifying body weight (optionally combined with known
CC medicaments), for treating diabetes, high blood pressure or high
CC cholesterol. The DNA encoding this sequence (and sequences complementary
CC to it) can be used in gene therapy for modifying body weight. This
CC protein can be used for reducing weight for health or cosmetic reasons in
CC obese humans, or to produce leaner food animals. Antagonists of OBP
CC (including antibodies) are useful for increasing body weight, e.g. for
CC treating weight loss associated with cancer, or for cosmetic reasons in
CC humans, or for production of Kobe beef or Foie gras in domestic animals.
CC OBP antibodies (Ab) can also be used in diagnostic immunoassays for the
CC presence of OBP. The formation of Ab-OBP complexes enables in vitro
CC evaluation of levels of OBP in a sample, especially to detect diseases
CC associated with elevated or decreased levels, and to monitor treatment of
CC these diseases

XX SQ Sequence 166 AA;

Query Match 100.0%; Score 731; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 2.1e-72;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKKQVGTGLDFIPGLHPILTLKMDQTLAVY 60

Db 22 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKKQVGTGLDFIPGLHPILTLKMDQTLAVY 81

Qy 61 QQILTSMPSRNVIQISNDLENLRLDLHLVLAFAFSKCHLPWASGLTDLDSLGGLVLEASGYST 120

Db 82 QQILTSMPSRNVIQISNDLENLRLDLHLVLAFAFSKCHLPWASGLTDLDSLGGLVLEASGYST 141

Qy 121 EVVALSRLOGLQDMLWQLDLSGPC 145

Db 142 EVVALSRLOGLQDMLWQLDLSGPC 166

Search completed: May 4, 2006, 21:52:16

Job time : 139.526 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 21:50:51 ; Search time 27.4055 Seconds
(without alignments)
509.074 Million cell updates/sec

Title: US-10-623-189-2

Perfect score: 731
Sequence: 1 VPIQKVQDDTKTLIKTIVTR.....SRLQGSIQDMLQDLSPGC 145

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_80:*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	731	100.0	166	2	I53166	leptin precursor -
2	720.5	98.6	167	1	LTHU	leptin precursor -
3	603.5	82.6	167	1	LTHU	leptin precursor -
4	589.5	80.6	167	1	LTRT	leptin precursor -
5	589.5	80.6	167	2	I55622	rat ob - rat
6	83	11.4	1600	2	A83281	phenylalanine-tRNA
7	82.5	11.3	790	2	H71509	probable myosin he
8	81.5	11.1	829	2	T01362	hypothetical prote
9	79	10.8	952	2	H84583	sensory transducti
10	78	10.7	420	2	S75514	probable membrane
11	78	10.7	674	2	S46092	conserved hypothet
12	77.5	10.6	186	2	G82638	phosphotransferase
13	77.5	10.6	574	1	B42374	internalin, peptid
14	77.5	10.6	821	2	B41126	hypothetical prote
15	77	10.5	444	2	S54039	hypothetical prote
16	77	10.5	1228	2	S46754	carbamoyl-phosphat
17	76.5	10.5	362	2	A83967	probable trehalose
18	76.5	10.5	822	2	E86305	probable soluble 1
19	75.5	10.3	639	2	A20055	maltose ABC transp
20	75	10.3	823	2	H72282	beta transducin-l1
21	75	10.3	1191	2	S76414	probable membrane
22	75	10.3	1438	2	S59792	hypothetical prote
23	74	10.1	403	2	T26551	prolactin, 20K - M
24	73.5	10.1	177	2	A28106	5,10-methylenetet
25	73.5	10.1	296	2	D70424	ATP-dependent RNA
26	73.5	10.1	296	2	D88511	hypothetical prote
27	73.5	10.1	348	2	A02247	protein-tyrosine-p
28	73.5	10.1	521	1	A44267	hypothetical prote
29	73.5	10.1	696	2	S44912	

ALIGNMENTS

RESULT 1

I53166

leptin precursor - human

N;Alternate names: obese

C;Species: Homo sapiens (man)

C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004

C;Accession: I53166; G02328

R;Masuzaki, H.; Ogawa, Y.; Isse, N.; Satoh, N.; Okazaki, T.; Shigemoto, M.; Mori, K.;

Diabetes 44, 855-858, 1995

A;Title: Human obese gene expression. Adipocyte-specific expression and regional differ

A;Reference number: I53166; MUID:95309556; PMID:7789654

A;Accession: I53166

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-166 <RES>

A;Cross-references: UNIPROT:P41159; UNIPARC:UPI000014D164; GB:D49487; NID:g904211; PID:

R;Chehab, F.F.; Lim, M.E.

submitted to the EMBL Data Library, December 1995

A;Reference number: H01063

A;Accession: G02328

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-166 <CHE>

A;Cross-references: UNIPARC:UPI000014D164; EMBL:U43415; NID:g1163105; PIDN:AAC31660.1;

C;Genetics:

A;Gene: GDB:LBP; OB; OBS

A;Cross-references: GDB:136420; OMIM:164160

A;Map position: 7q32.1-7q32.1

A;Introns: 48/3

C;Superfamily: leptin

Query Match 100.0%; Score 731, DB 2; Length 166;

Best Local Similarity 100.0%; Pred. No. 2.2e-59;

Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKQKVGTGLDFIPGLHPILTLKMDQTLAVY 60

DB 22 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKQKVGTGLDFIPGLHPILTLKMDQTLAVY 81

QY 61 QQILTSPSRNVIQISNDLENLRDLHLVAFPSKSHLPWASGLETLDLSLGVLEASGYST 120

DB 82 QQILTSPSRNVIQISNDLENLRDLHLVAFPSKSHLPWASGLETLDLSLGVLEASGYST 141

QY 121 EWALSRQGSIQDMLQDLSPGC 145

DB 142 EWALSRQGSIQDMLQDLSPGC 166

RESULT 2

LTHU

leptin precursor - human

N;Alternate names: obese protein; obesity factor

C;Species: Homo sapiens (man)
C;Date: 28-Jul-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: A38952; JEO148
R;Zhang, Y.; Proenca, R.; Maffei, M.; Barone, M.; Leopold, L.; Friedman, J.M.
Nature 372, 425-432, 1994
A;Title: Positional cloning of the mouse obese gene and its human homologue.
A;Reference number: S50863; MUID:95075453; PMID:7984236
A;Accession: A38952
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-167 <ZHA>
A;Cross-references: UNIPROT:P41159; UNIPARC:UPI00000308D4; GB:U18915; NID:G623331; PIDN:
R;Liao, H.J.; Deng, Y.B.; Chen, X.M.; Ye, Y.Z.
Chinese Biochem. J. 13, 249-253, 1997
A;Title: Cloning of Chinese obesity gene and construction of prokaryotic expression vec
A;Reference number: JEO148
A;Accession: JEO148
A;Molecule type: mRNA
A;Residues: 'M', 22-167 <LIA>
A;Cross-references: UNIPARC:UPI0000158347
A;Experimental source: adipose
A;Note: the author translated GAC for residue 148 as Ser
C;Genetics:
A;Gene: GDB:LEP; OB; OBS
A;Cross-references: GDB:136420; OMIM:164160
A;Map position: 7q31.3-7q31.3
C;Superfamily: leptin
C;Keywords: adipose tissue
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-167/Product: leptin #status predicted <MAT>

Query Match 98.6%; Score 720.5; DB 1; Length 167;
Best Local Similarity 99.3%; Pred. No. 28-58; Mismatches 0; Indels 1; Gaps 1;
Matches 145; Conservative 0;

QY 1 VPIQKVDDTKTIKTIIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 59
Db 22 VPIQKVDDTKTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 81

QY 60 YQILTSMPSRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSIGGVLEASGYS 119
Db 82 YQILTSMPSRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSIGGVLEASGYS 141

QY 120 TEVALSRLOGLQSLQDMLWQDLSPGC 145
Db 142 TEVALSRLOGLQSLQDMLWQDLSPGC 167

RESULT 3
LTVS
leptin precursor - mouse
N;Alternate names: obese protein
C;Species: Mus musculus (house mouse)
C;Date: 14-Jul-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: S50863
R;Zhang, Y.; Proenca, R.; Maffei, M.; Barone, M.; Leopold, L.; Friedman, J.M.
Nature 372, 425-432, 1994
A;Title: Positional cloning of the mouse obese gene and its human homologue.
A;Reference number: S50863; MUID:95075453; PMID:7984236
A;Accession: S50863
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-167 <ZHA>
A;Cross-references: UNIPROT:P41160; UNIPARC:UPI00000308D4; EMBL:U18812; NID:G746416; PIDN:
C;Superfamily: leptin
C;Keywords: adipose tissue
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-167/Product: leptin #status predicted <MAT>

Query Match 82.6%; Score 603.5; DB 1; Length 167;
Best Local Similarity 84.2%; Pred. No. 9e-48; Mismatches 13; Indels 1; Gaps 1;
Matches 123; Conservative 13;

QY 1 VPIQKVDDTKTIKTIIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 59
Db 22 VPIQKVDDTKTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 81

QY 60 YQILTSMPSRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSIGGVLEASGYS 119
Db 82 YQILTSMPSRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSIGGVLEASGYS 141

QY 120 TEVALSRLOGLQSLQDMLWQDLSPGC 145
Db 142 TEVALSRLOGLQSLQDMLWQDLSPGC 167

RESULT 4
LTVT
leptin precursor - rat
N;Alternate names: obese protein; obesity factor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Jul-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: PC4034; JC4142
R;Funahashi, T.; Shimomura, I.; Hiraoka, H.; Arai, T.; Takahashi, M.; Nakamura, T.; Noz
Biochem. Biophys. Res. Commun. 211, 469-475, 1995
A;Title: Enhanced expression of rat obese (ob) gene in adipose tissues of ventromedial
A;Reference number: PC4034; MUID:95314614; PMID:7794258
A;Accession: PC4034
A;Molecule type: mRNA
A;Residues: 1-167 <FUN>
A;Cross-references: UNIPROT:P50596; UNIPARC:UPI0000038DAF
A;Experimental source: adipose tissue
A;Note: The authors translated the codon AAA for residue 32 as Thr
R;Murakami, T.; Shima, K.
Biochem. Biophys. Res. Commun. 209, 944-952, 1995
A;Title: Cloning of rat obese cDNA and its expression in obese rats.
A;Reference number: JC4142; MUID:95251725; PMID:7733988
A;Accession: JC4142
A;Molecule type: mRNA
A;Residues: 1-167 <MUR>
A;Cross-references: UNIPARC:UPI0000038DAF; DDBJ:D49653; NID:G995614; PIDN:BA08529.1; P
A;Experimental source: liver
C;Comment: This protein is proposed to function as part of a signalling pathway from ad
C;Genetics:
A;Gene: obese
C;Superfamily: leptin
C;Keywords: adipose tissue
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-167/Product: leptin #status predicted <MAT>

Query Match 80.6%; Score 589.5; DB 1; Length 167;
Best Local Similarity 82.9%; Pred. No. 1.7e-46; Mismatches 11; Indels 1; Gaps 1;
Matches 121; Conservative 13;

QY 1 VPIQKVDDTKTIKTIIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 59
Db 22 VPIQKVDDTKTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 81

QY 60 YQILTSMPSRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSIGGVLEASGYS 119
Db 82 YQILTSMPSRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSIGGVLEASGYS 141

QY 120 TEVALSRLOGLQSLQDMLWQDLSPGC 145
Db 142 TEVALSRLOGLQSLQDMLWQDLSPGC 167

RESULT 5
I55622
rat ob - rat
C;Species: Rattus sp. (rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C;Accession: I55622
R;Ogawa, Y.; Maizaki, H.; Isse, N.; Okazaki, T.; Mori, K.; Shigemoto, M.; Satoh, N.; T
J. Clin. Invest. 96, 1647-1652, 1995

A;Title: Molecular cloning of rat obese cDNA and augmented gene expression in genetically
A;Reference number: I55622; MUID:95386724; PMID:7657834
A;Accession: I55622
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-167 <RES>
A;Cross-references: UNIPARC:UPI0000038DAF; GB:D45862; NID:g1018990; PIDN:BAA08296.1; PID
C;Superfamily: leptin

Query Match 80.6%; Score 589.5; DB 2; Length 167;
Best Local Similarity 82.9%; Pred. No. 1.7e-46; Indels 1; Gaps 1;
Matches 121; Conservative 13; Mismatches 11;

Qy 1 VPIQVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTSKMDQTLAV 59

Db 22 VPIHKVQDDTKTLIKTIVTRINDISHTQSVARQVGTGLDFIPGLHPILTSKMDQTLAV 81

Qy 60 YQILTSMPGRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDLSGGVLEASGYS 119

Db 82 YQILTSMPGRNVQISNDLENRLDLHLVAFSKSCHLPQTRGLQKPSLDGVLASLYS 141

Qy 120 TEVVALSRLOGSLQDMLWQDLSPGC 145

Db 142 TEVVALSRLOGSLQDILQQLDLSPEC 167

RESULT 6

AB3281 glutamate dehydrogenase (EC 1.4.1.2) [imported] - Brucella melitensis (strain 16M)

C;Species: Brucella melitensis

C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 05-Oct-2004

C;Accession: AB3281

R;DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, A.; Mazur, M.; Goldsman, E.; Seikov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis

A;Reference number: AD3252; PMID:11756688

A;Accession: AB3281

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1600 <CUR>

A;Cross-references: UNIPROT:Q8YJ55; UNIPARC:UPI0000057BD4; GB:AE008917; PIDN:AAL51413.1;

A;Superfamily: glutamate dehydrogenase, Mll4104 type

C;Genetics:

A;Gene: BMEI0231

A;Map position: 1

C;Superfamily: glutamate dehydrogenase, Mll4104 type

C;Keywords: oxidoreductase

Query Match 11.4%; Score 83; DB 2; Length 1600;

Best Local Similarity 25.6%; Pred. No. 38;

Matches 33; Conservative 22; Mismatches 52; Indels 22; Gaps 5;

Qy 6 VQDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTSKMDQTLAVYQILTL 65

Db 97 VNDNMPFLDSIMGELND--HTS-----QIFMVVHPVLDISREKDELVLGEASQ 144

Qy 66 SMPGRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDLSGGVLEASGYSTEVVAL 125

Db 145 LAPAKGVRS-----LVQIHLPALSKQAKADTAGLKR--LGQV--RSASVDWKPM 194

Qy 126 SRLQSLQD 134

Db 195 KRLDGAIDD 203

RESULT 7

H71509

phenylalanine-tRNA ligase (EC 6.1.1.20) beta chain - Chlamydia trachomatis (serotype D,

C;Species: Chlamydia trachomatis

C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004

C;Accession: H71509

R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,

Science 282, 754-759, 1998

A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra

A;Reference number: A71570; MUID:99000809; PMID:9784136

A;Accession: H71509

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-790 <ARN>

A;Cross-references: UNIPROT:O84481; UNIPARC:UPI0000136445; GB:AE001321; GB:AE001273; NI

A;Experimental source: serotype D, strain UW-3/Cx

C;Genetics:

A;Gene: pheT

C;Superfamily: phenylalanine-tRNA ligase beta chain

C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 11.3%; Score 82.5; DB 2; Length 790;

Best Local Similarity 27.5%; Pred. No. 17;

Matches 46; Conservative 26; Mismatches 54; Indels 41; Gaps 10;

Qy 2 PIQKVQDDTKTLI-----KTIIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTSKMDQ 55

Db 395 PIQKIGDDSPSLSVRPKTI-KRLDIELSTAEIVAKLSSLSGF-----Q 439

Qy 56 TLAVYQQILTSMPS--RNVIQISNDLENRLDLHLVAFSKSCH--LPWASGLETLD----- 107

Db 440 TAVEEQAVRVEVFSYRHDIQEETDL--VEICRTTPFVKQTKILPTTPTIYSLKRELT 497

Qy 108 --SLGGVLEASGYS---TEVVALSRLOGSL---QDMLWQL--DLSPG 144

Db 498 FLANGGLQFFTYSLDTEVSSLSQESSLIPVQNSSWKLRLDLSLPG 544

RESULT 8

T01362

probable myosin heavy chain At2g34730 - Arabidopsis thaliana

N;Alternate names: hypothetical protein T29F13.6

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004

C;Accession: T01362; C84760

R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kan

submitted to the EMBL Data Library, May 1998

A;Description: Arabidopsis thaliana chromosome II BAC T29F13 genomic sequence.

A;Reference number: 214179

A;Accession: T01362

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-829 <ROU>

A;Cross-references: UNIPROT:O64584; UNIPARC:UPI000004A13E; EMBL:AC003096; NID:g3132469;

A;Experimental source: cultivar Columbia

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, J.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: C84760

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-829 <STO>

A;Cross-references: UNIPARC:UPI000004A13E; GB:AE002093; NID:g3132472; PIDN:AAC16261.1;

C;Genetics:

A;Gene: At2g34730; T29F13.6

A;Map position: 2

A;Introns: 728/2; 770/3

Query Match 11.1%; Score 81.5; DB 2; Length 829;

Best Local Similarity 21.0%; Pred. No. 23;

Matches 33; Conservative 27; Mismatches 46; Indels 51; Gaps 5;

Qy 3 IQKVQDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTSKMDQTLAVY-- 60

Db 57 ISRVVSD--SIIRGVWTAIESDAEAKIAQKD-----LELSKIRETLVYV 100

Qy 61 -----QQILTSMPGRNVQISNDLENRLDLHLVAFSKSCHLPW 99

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 21:47:48 ; Search time 144.502 Seconds
(without alignments)
707.961 Million cell updates/sec

Title: US-10-623-189-2

Perfect score: 731

Sequence: 1 VPIQKVQDDTKLIKTIIVTR.....SRLLQGSILQDMLWLQSLSPGC 145

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	720.5	98.6	167	1	P41159 homo sapien
2	720.5	98.6	167	1	O6NT58 HUMAN
3	717.5	98.2	146	1	OB_PANTR
4	712.5	97.5	146	1	OB_GORGO
5	705.5	96.5	146	1	OB_PONPY
6	656.5	89.8	167	1	OB_MACMU
7	623.5	85.3	167	1	OB_FELCA
8	612.5	83.8	146	2	O6T8R8 BUBBU
9	612.5	83.8	167	1	OB_BOVIN
10	612.5	83.8	167	1	OB_BUBBU
11	611.5	83.7	167	1	OB_PIG
12	611.5	83.7	167	2	O5TIL9 PTG
13	608.5	83.2	146	1	OB_SHEEP
14	608.5	83.2	167	2	O5EAE4 BOVIN
15	603.5	82.6	146	2	O4VW71_CTEID
16	603.5	82.6	167	1	OB_MOUSE
17	603.5	82.6	167	2	O544U0 MOUSE
18	599.5	82.0	146	2	O4VW70_HYPMO
19	599.5	82.0	146	2	O4VW72_CARAU
20	599.5	82.0	146	2	O4L1M8_CYPCA
21	597	81.7	163	1	OB_CHICK
22	596.5	81.6	146	2	O4VM67 MEGAM
23	593.5	81.2	146	2	O4VM68_SILAS
24	589.5	80.6	167	1	OB_RAT
25	588.5	80.5	146	2	O4VM66_9PERC
26	588.5	80.5	146	2	O4VM81_9TELE
27	588	80.4	147	2	O4VM60_ANAPL
28	587	80.3	145	1	OB_MEIGA
29	581.5	79.5	146	2	O4VM69_ARINO
30	580.5	79.4	167	1	OB_CANFA
31	507	69.4	145	1	OB_HORSE

32	495.5	67.8	167	1	OB_SMICR
33	493	67.4	119	2	O861R2_BUBBU
34	483.5	66.1	118	2	O4VYB6_9RODE
35	477	65.3	118	2	O8MK60_ALOLA
36	476	65.1	118	2	O8MK58_VULVU
37	474	64.8	118	2	O8MK59_NYCPR
38	469	64.2	118	2	O8MK61_CANFA
39	457	62.5	110	2	O56QF8_SHEEP
40	450.5	61.6	123	2	O95KW9_MYOLU
41	449.5	61.5	167	1	OB_HALGR
42	447.5	61.2	167	1	OB_PHOVI
43	444	60.7	109	2	O866S7_BUBBU
44	434	59.4	109	2	O864V1_CAMDR
45	387	52.9	106	2	O95MG5_CAPHI

ALIGNMENTS

RESULT 1
OB_HUMAN STANDARD; PRT; 167 AA.
ID OB_HUMAN
AC P41159, O15158; O56A88;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Leptin precursor (Obesity factor) (Obese protein).
GN Name=LEP; Synonyms=OB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE
RA MEDLINE=95075453; PubMed=7984236; DOI=10.1038/372425a0;
RX Zhang Y., Proenca P., Maffei M., Barone M., Leopold L., Friedman J.M.;
RT "Positional cloning of the mouse obese gene and its human homologue.";
RL Nature 372:425-432(1994).
RN [2]
RP ERRATUM.
RA Zhang Y., Proenca P., Maffei M., Barone M., Leopold L., Friedman J.M.;
RL Nature 374:479-479(1995).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95309556; PubMed=7789654;
RA Masuzaki H., Ogawa Y., Isse N., Satoh N., Okazaki T., Shigemoto M.,
RA Mori K., Tamura N., Hosoda K., Yoshimasa Y., Jingami H., Kawada T.,
RA Nakao K.;
RT "Human obese gene expression. Adipocyte-specific expression and
regional differences in the adipose tissue.";
RL Diabetes 44:855-858(1995).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96223958; PubMed=8626726; DOI=10.1074/jbc.271.8.3971;
RA Gong D.W., Bi S., Pratley R.E., Weintraub B.D.;
RT "Genomic structure and promoter analysis of the human obese gene.";
RL J. Biol. Chem. 271:3971-3974(1996).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96070903; PubMed=7499240; DOI=10.1074/jbc.270.46.27728;
RA Isse N., Ogawa Y., Tamura N., Masuzaki H., Mori K., Okazaki T.,
RA Satoh N., Shigemoto M., Yoshimasa Y., Nishi S., Hosoda K., Inazawa J.,
RA Nakao K.;
RT "Structural organization and chromosomal assignment of the human obese
gene.";
RL J. Biol. Chem. 270:27728-27733(1995).
RN [7]
RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=96198511; PubMed=8621021;
 RA Niki T., Mori H., Tamori Y., Kiehimoto-Haehitamoto M., Ueno H.,
 RA Araki S., Maugi J., Sawant N., Majithia H.R., Rais N.,
 RA Hashimoto M., Taniguchi H., Kasuga M.;
 RT "Human obese gene: molecular screening in Japanese and Asian Indian
 RT NIDDM patients associated with obesity.";
 RL Diabetes 45:675-678(1996).
 RN [6]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RA Lu L., Fu Z., Xu M., Fu Y., Hu Z.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANT MET-94.
 RA Bieder M.J., Johanson E.J., da Ponte S.H., Hastings N.C., Ahearn M.O.,
 RA Bertucci C.B., Wong M.W., Yi Q., Nickerson D.A.;
 RT "SeattlesNP8. NHLBI HUG6662 program for genomic applications, UW-
 RT FRCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 RN [10]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Placenta;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uadin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [11]
 RP INTERACTION WITH SIGLEC6.
 RX MEDLINE=99357812; PubMed=10428856; DOI=10.1074/jbc.274.32.22729;
 RA Patel N., Brinkman-Van der Linden E.C.M., Altmann S.W., Gish K.C.,
 RA Balasubramanian S., Timans J.C., Peterson D., Bell M.P., Bazan J.F.,
 RA Varki A., Kastelein R.A.;
 RT "OB-BP1/Siglec-6. A leptin- and sialic acid-binding protein of the
 RT immunoglobulin superfamily.";
 RL J. Biol. Chem. 274:22729-22738(1999).
 RN [12]
 RP ERRATUM.
 RA Patel N., Brinkman-Van der Linden E.C.M., Altmann S.W., Gish K.C.,
 RA Balasubramanian S., Timans J.C., Peterson D., Bell M.P., Bazan J.F.,
 RA Varki A., Kastelein R.A.;
 RL J. Biol. Chem. 274:28058-28058(1999).
 RN [13]
 RP STRUCTURE BY NMR.
 RX MEDLINE=97309492; PubMed=9166907; DOI=10.1016/S0014-5793(97)00353-0;
 RA Kline A.D., Becker G.W., Churgay L.M., Landen B.E., Martin D.K.,
 RA Muth W.L., Rathnachalam R., Richardson J.M., Schoner B., Ulmer M.,
 RA Hale J.E.;
 RT "Leptin is a four-helix bundle: secondary structure by NMR.";
 RL FEBS Lett. 407:239-242(1997).
 RN [14]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ÅNGSTRÖMS).
 RX MEDLINE=97289390; PubMed=9144295;
 RA Zhang F., Basinski M.B., Beals J.M., Briggs S.L., Churgay L.M.,
 RA Clawson D.K., Dimarchi R.D., Furman T.C., Hale J.E., Heiling H.M.,
 RA Schoner B.E., Smith D.P., Zhang X.Y., Wery J.P., Schevitz R.W.;
 RT "Crystal structure of the obese protein leptin-E100.";
 RL Nature 387:206-209(1997).

RN [15]
 RP VARIANT MET-94.
 RA Bartholomew D.W., McClellan J.M.;
 RT "A novel polymorphism in the leptin gene.";
 RL Hum. Mutat. 12:220-220(1998).
 RN [16]
 RP VARIANT MORBID OBESITY TRP-105.
 RX MEDLINE=98160176; PubMed=9500540;
 RA Strobel A., Issad T., Camoin L., Ozata M., Strosberg A.D.;
 RT "A leptin missense mutation associated with hypogonadism and morbid
 RT obesity.";
 RL Nat. Genet. 18:213-215(1998).
 CC -I- FUNCTION: May function as part of a signaling pathway that acts to
 CC regulate the size of the body fat depot. An increase in the level
 CC of LEPTIN may act directly or indirectly on the CNS to inhibit food
 CC intake and/or regulate energy expenditure as part of a homeostatic
 CC mechanism to maintain constancy of the adipose mass.
 CC -I- SUBUNIT: Interacts with SIGLEC6.
 CC -I- SUBCELLULAR LOCATION: Secreted.
 CC -I- DISEASE: Defects in LEPTIN may be a cause of autosomal recessive
 CC obesity [MIM:601665].
 CC -I- SIMILARITY: Belongs to the leptin family.
 CC -I- DATABASES: NAME=Ref Systems' cytokine mini-reviews: LEP;
 CC WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyid=213".
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; U18915; AAA0470.1; -; mRNA.
 DR EMBL; D49487; BAA08448.1; -; mRNA.
 DR EMBL; U43653; AAC50400.1; -; mRNA.
 DR EMBL; U43415; AAC31660.1; -; Genomic DNA.
 DR EMBL; D63710; BAA09839.1; -; Genomic DNA.
 DR EMBL; D63519; BAA09787.1; -; Genomic DNA.
 DR EMBL; AF008123; AAB63507.1; -; mRNA.
 DR EMBL; AY996373; AAX81413.1; -; Genomic DNA.
 DR EMBL; BC060830; AAB60830.1; -; mRNA.
 DR EMBL; BC069452; AAB69452.1; -; mRNA.
 DR EMBL; BC069527; AAB69527.1; -; mRNA.
 DR PIR; A38952; LTHU
 DR PIR; I53166; -;
 DR PDB; IAX8; X-ray; @=22-167.
 DR Ensembl; ENSG0000174697; Homo sapiens.
 DR HGNC; HGNC:6553; LEP.
 DR MIM; 164160; -;
 DR MIM; 601665; -;
 DR GO; GO:0005615; Cytoplasmic space; TAS.
 DR GO; GO:0006112; P:energy reserve metabolism; TAS.
 DR InterPro; IPR012351; Cytokine_4_hlx.
 DR InterPro; IPR000065; Leptin.
 DR PANTHER; PTHR11724; Leptin; 1.
 DR Pfam; PF02024; Leptin; 1.
 DR PRINTS; PF00495; LEPTIN.
 DR PRODOM; PD005698; Leptin; 1.
 DR 3D-structure; Diabetes mellitus; Disease mutation; Obesity;
 KW Polymorphism; Signal.
 FT SIGNAL 1 21 Potential.
 FT CHAIN 22 167 Leptin.
 FT DISULFID 117 167
 FT VARIANT 49 49
 FT VARIANT 94 94 Missing (in 30% the clones).
 FT VARIANT 105 105 V -> M (in dbSNP:17151919).
 FT VARIANT 110 110 /FTId=VAR 004196.
 FT VARIANT 96 96 V -> W (in morbid obesity and
 FT VARIANT 25 44 hypogonadism).
 FT VARIANT 110 110 /FTId=VAR 008094.
 FT VARIANT 96 96 V -> M (in dbSNP:1800564).
 FT CONFLICT 96 96 Q -> R (in Ref. 8).
 FT HELIX 25 44


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FT HELIX 72 87
FT TURN 88 88

Query Match 98.6%; Score 720.5; DB 1; Length 167;
Best Local Similarity 99.3%; Pred. No. 2.1e-58;
Matches 145; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 VPIQKVQDDTKTLIKITVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 59
DB 22 VPIQKVQDDTKTLIKITVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 81

QY 60 YQIILTSMPNRNVIQISNDLENLRLDLHLVLAFSKSLPWSAGLETLDLSGGVLEASGYS 119
DB 82 YQIILTSMPNRNVIQISNDLENLRLDLHLVLAFSKSLPWSAGLETLDLSGGVLEASGYS 141

QY 120 TEVVALSRLOGLQDMLWQLDLSGCG 145
DB 142 TEVVALSRLOGLQDMLWQLDLSGCG 167

RESULT 2
Q6NT58 HUMAN
ID Q6NT58 HUMAN PRELIMINARY; PRT; 167 AA.
AC Q6NT58;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Leptin,
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuller G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzanski M.I., Skalska U., Smailus D.B.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences".
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RA Strausberg R.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May function as part of a signaling pathway that acts to
CC regulate the size of the body fat depot. An increase in the level
CC of LEP may act directly or indirectly on the CNS to inhibit food
CC intake and/or regulate energy expenditure as part of a homeostatic
CC mechanism to maintain constancy of the adipose mass (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC EMBL; BC069323; AA069323.1; -; mRNA.
CC HSSP; P41159; IAX8.
CC RHA; 24-167.
CC SMR; Q6NT58; 24-167.
```

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DR Ensembl; ENSG00000174697; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; P:hormone activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR012351; Cytokine_4_hlx.
DR InterPro; IPR000065; Leptin.
DR Pfam; PF02024; Leptin.1.
DR PRINTS; PR00495; LEPTIN.
DR PRODOM; PD005698; Leptin; 1.
SQ SEQUENCE 167 AA; 18613 MW; BE1A046FBF1554DE CRC64;

Query Match 98.6%; Score 720.5; DB 2; Length 167;
Best Local Similarity 99.3%; Pred. No. 2.1e-58;
Matches 145; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 VPIQKVQDDTKTLIKITVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 59
DB 22 VPIQKVQDDTKTLIKITVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 81

QY 60 YQIILTSMPNRNVIQISNDLENLRLDLHLVLAFSKSLPWSAGLETLDLSGGVLEASGYS 119
DB 82 YQIILTSMPNRNVIQISNDLENLRLDLHLVLAFSKSLPWSAGLETLDLSGGVLEASGYS 141

QY 120 TEVVALSRLOGLQDMLWQLDLSGCG 145
DB 142 TEVVALSRLOGLQDMLWQLDLSGCG 167

RESULT 3
OB_PANTR
ID OB_PANTR STANDARD; PRT; 146 AA.
AC O02750;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Leptin (Obesity factor).
GN Name=LEP; Synonyms=OB;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pan.
OX NCBI_TaxID=9598;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Schoner B., Basinski M.B., Smith D.P., Hsiung H.M., Zhang X.,
RA Rockey P.K., Rostek P.R.;
RT "Cloning of obese genes from different species: a comparison of the
RT gene structures and the sequences of the obese gene products,
RT leptin."
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May function as part of a signaling pathway that acts to
CC regulate the size of the body fat depot. An increase in the level
CC of LEP may act directly or indirectly on the CNS to inhibit food
CC intake and/or regulate energy expenditure as part of a homeostatic
CC mechanism to maintain constancy of the adipose mass (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- SIMILARITY: Belongs to the leptin family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; U96450; AB54023.1; -; mRNA.
CC HSSP; P41159; IAX8.
CC SMR; O02750; 3-146.
CC InterPro; IPR012351; Cytokine_4_hlx.
CC InterPro; IPR000065; Leptin.
CC PANTHER; PTHR11724; Leptin; 1.
CC Pfam; PF02024; Leptin; 1.
CC PRINTS; PR00495; LEPTIN.
```

DR ProDom; PD005698; Leptin; 1.
 KW Obesity. 96 146 By similarity.
 FT DISULFID 146 AA; 16059 MW; 02C42A08554D55C CRC64;
 -SQ SEQUENCE 146 AA; 16059 MW; 02C42A08554D55C CRC64;
 Query Match 98.2%; Score 717.5; DB 1; Length 146;
 Best Local Similarity 98.6%; Pred. No. 3.4e-58;
 Matches 144; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
 QY 1 VPIQKVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 59
 DB 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSQKQVTGLDFIPGLHPILTLKMDQTLAV 60
 QY 60 YQILTSMPSRNVIQISNDLENRLDLHLAFSKSCHLPWASGLTLDLSGGVLEASGYS 119
 DB 61 YQILTSMPSRNVIQISNDLENRLDLHLAFSKSCHLPWASGLTLDLSGGVLEASGYS 120
 QY 120 TEVVALSRQSGSLQDMLWQLDLSPGC 145
 DB 121 TEVVALSRQSGSLQDMLWQLDLSPGC 146
 RESULT 4
 OB_GORGO
 ID OB_GORGO STANDARD; PRT; 146 AA.
 AC Q95189;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Leptin (Obesity factor).
 GN Names=LEP; Synonyms=OB;
 OS Gorilla gorilla gorilla (Lowland gorilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Gorilla.
 OX NCBI_TaxID=9595;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RA Smith D.P., Zhang X., Hsiung H.M.;
 RT "Gorilla leptin genomic sequence."
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: May function as part of a signaling pathway that acts to
 CC regulate the size of the body fat depot. An increase in the level
 CC of LEP may act directly or indirectly on the CNS to inhibit food
 CC intake and/or regulate energy expenditure as part of a homeostatic
 CC mechanism to maintain constancy of the adipose mass (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -!- SIMILARITY: Belongs to the leptin family.
 CC -----
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; U72872; AAB17091.1; -; Genomic_DNA.
 CC HSSP; P41159; IAX8.
 CC SNR; Q95189; 3-146.
 CC InterPro; IPR012351; Cytokine_4_hlx.
 CC InterPro; IPR000065; Leptin.
 CC PANTHER; PTHR11724; Leptin; 1.
 CC Pfam; PF02024; Leptin; 1.
 CC PRINTS; PR00495; LEPTIN.
 CC ProDom; PD005698; Leptin; 1.
 CC KW Obesity.
 FT DISULFID 96 146 By similarity.
 SQ SEQUENCE 146 AA; 16031 MW; 02C43BF68B4C85C CRC64;
 Query Match 97.5%; Score 712.5; DB 1; Length 146;
 Best Local Similarity 97.9%; Pred. No. 9.8e-58;
 Matches 143; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 1 VPIQKVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 59
 DB 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSQKQVTGLDFIPGLHPILTLKMDQTLAV 60
 QY 60 YQILTSMPSRNVIQISNDLENRLDLHLAFSKSCHLPWASGLTLDLSGGVLEASGYS 119
 DB 61 YQILTSMPSRNVIQISNDLENRLDLHLAFSKSCHLPWASGLTLDLSGGVLEASGYS 120
 QY 120 TEVVALSRQSGSLQDMLWQLDLSPGC 145
 DB 121 TEVVALSRQSGSLQDMLWQLDLSPGC 146
 RESULT 5
 OB_PONPY
 ID OB_PONPY STANDARD; PRT; 146 AA.
 AC Q95234;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Leptin (Obesity factor).
 GN Names=LEP; Synonyms=OB;
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Pongo.
 OX NCBI_TaxID=9600;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Schoner B., Basinski M.B., Smith D.P., Hsiung H.M., Zhang X.,
 RA Rokeby P.K., Rostek P.R.;
 RT "Cloning of obese genes from different species: a comparison of the
 RT gene structures and the sequences of the obese gene products,
 RT leptin."
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: May function as part of a signaling pathway that acts to
 CC regulate the size of the body fat depot. An increase in the level
 CC of LEP may act directly or indirectly on the CNS to inhibit food
 CC intake and/or regulate energy expenditure as part of a homeostatic
 CC mechanism to maintain constancy of the adipose mass (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -!- SIMILARITY: Belongs to the leptin family.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; U72873; AAB17092.1; -; Genomic_DNA.
 CC HSSP; P41159; IAX8.
 CC SNR; Q95234; 3-146.
 CC InterPro; IPR012351; Cytokine_4_hlx.
 CC InterPro; IPR000065; Leptin.
 CC PANTHER; PTHR11724; Leptin; 1.
 CC Pfam; PF02024; Leptin; 1.
 CC PRINTS; PR00495; LEPTIN.
 CC ProDom; PD005698; Leptin; 1.
 CC KW Obesity.
 FT DISULFID 96 146 By similarity.
 SQ SEQUENCE 146 AA; 16195 MW; 3F50A13338FDBD4 CRC64;
 Query Match 96.5%; Score 705.5; DB 1; Length 146;
 Best Local Similarity 96.6%; Pred. No. 4.3e-57;
 Matches 141; Conservative 2; Mismatches 2; Indels 1; Gaps 1;
 QY 1 VPIQKVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 59
 DB 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSQKQVTGLDFIPGLHPILTLKMDQTLAV 60
 QY 60 YQILTSMPSRNVIQISNDLENRLDLHLAFSKSCHLPWASGLTLDLSGGVLEASGYS 119

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Db 61 YQOILTMPSRNVQISNDLENLRLHLVLAFAKSKCHLPWASGLTDLRLGGLVLEASGYS 120
120 TEVVALSRLOGLQSLQDMLWQLDLSFGC 145
121 TEVVALSRLOGLQSLQDMLWQLDLSFGC 146

RESULT 6
OB_MACMU
ID OB_MACMU STANDARD; PRT; 167 AA.
AC Q28504;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Leptin precursor (Obesity factor).
GN Name=LEP; Synonyms=OB;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecidae; Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
NUCLEOTIDE SEQUENCE.
RP TISSUE=Adipose tissue;
RC MDLINE=96411743; PubMed=8810296; DOI=10.1074/jbc.271.41.25327;
RA Hotta K., Gustafson T.A., Ortmeier H.K., Bodkin N.L., Nicolson M.A.,
RA Hansen B.C.;
RT "Regulation of obese (ob) mRNA and plasma leptin levels in rhesus
RT monkeys. Effects of insulin, body weight, and non-insulin-dependent
RT diabetes mellitus."
RL J. Biol. Chem. 271:25327-25331(1996).
CC -1- FUNCTION: May function as part of a signaling pathway that acts to
CC regulate the size of the body fat depot. An increase in the level
CC of LEP may act directly or indirectly on the CNS to inhibit food
CC intake and/or regulate energy expenditure as part of a homeostatic
CC mechanism to maintain constancy of the adipose mass.
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- SIMILARITY: Belongs to the leptin family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; U58492; AAC50730.1; -; mRNA.
CC HSP; P41159; IAX8.
CC SMR; Q28504; 24-167.
CC InterPro; IPR012351; Cytokine 4_hlx.
CC PANTHER; PTHR11724; Leptin; 1.
CC Pfam; PF02024; Leptin; 1.
CC PRINTS; PR00495; LEPTIN.
CC ProDom; PD005698; Leptin; 1.
CC Obesity; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 167 Leptin.
FT DISULFID 117 167 By similarity.
FT SEQUENCE 167 AA; 18953 MW; E7D9F30628A5BBE9 CRC64;

Query Match 89.8%; Score 656.5; DB 1; Length 167;
Best Local Similarity 90.4%; Pred. No. 1.7e-52;
Matches 132; Conservative 8; Mismatches 5; Indels 1; Gaps 1;

; Qy 1 VPIQKVQDDTKTLIKTIIVTRINDISHT-SVSSKKQVTLGDFIPGLHPILTLSKMDQTLAV 59
Db 22 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKKQVTLGDFIPGLHPILTLSQMDQTLAI 81
Qy 60 YQOILTMPSRNVQISNDLENLRLHLVLAFAKSKCHLPWASGLTDLRLGGLVLEASGYS 119
Db 82 YQOILINLPSRNVQISNDLENLRLHLVLAFAKSKCHLPWASGLTDLRLGGLVLEASGYS 141
120 TEVVALSRLOGLQSLQDMLWQLDLSFGC 145
Qy 120 TEVVALSRLOGLQSLQDMLWQLDLSFGC 145

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Db 142 TEVVALSRLOGLQSLQDMLWQLDLSFGC 167

RESULT 7
OB_FELCA
ID OB_FELCA STANDARD; PRT; 167 AA.
AC Q292C1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Leptin precursor (Obesity factor).
GN Name=LEP; Synonyms=OB;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC Felinae; Felis.
OX NCBI_TaxID=9685;
RN [1]
NUCLEOTIDE SEQUENCE.
RP TISSUE=White adipose tissue;
RC Sasaki N., Iwase M., Kimura K., Ohishi I., Saito M.;
RT "Molecular cloning of feline leptin cDNA."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: May function as part of a signaling pathway that acts to
CC regulate the size of the body fat depot. An increase in the level
CC of LEP may act directly or indirectly on the CNS to inhibit food
CC intake and/or regulate energy expenditure as part of a homeostatic
CC mechanism to maintain constancy of the adipose mass (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- SIMILARITY: Belongs to the leptin family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AB0411360; BAA95481.1; -; mRNA.
CC HSP; P41159; IAX8.
CC SMR; Q292C1; 24-167.
CC InterPro; IPR012351; Cytokine 4_hlx.
CC InterPro; IPR000065; Leptin.
CC PANTHER; PTHR11724; Leptin; 1.
CC Pfam; PF02024; Leptin; 1.
CC PRINTS; PR00495; LEPTIN.
CC ProDom; PD005698; Leptin; 1.
CC Obesity; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 167 Leptin.
FT DISULFID 117 167 By similarity.
FT SEQUENCE 167 AA; 18584 MW; 643720DBB0AB4B95 CRC64;

Query Match 85.3%; Score 623.5; DB 1; Length 167;
Best Local Similarity 85.6%; Pred. No. 1.9e-49;
Matches 125; Conservative 11; Mismatches 9; Indels 1; Gaps 1;

Qy 1 VPIQKVQDDTKTLIKTIIVTRINDISHT-SVSSKKQVTLGDFIPGLHPILTLSKMDQTLAV 59
Db 22 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKKQVTLGDFIPGLHPILTLSKMDQTLAI 81
Qy 60 YQOILTMPSRNVQISNDLENLRLHLVLAFAKSKCHLPWASGLTDLRLGGLVLEASGYS 119
Db 82 YQOILTLGLPSRNVQISNDLENLRLHLVLAFAKSKCHLPWASGLTDLRLGGLVLEASGYS 141
120 TEVVALSRLOGLQSLQDMLWQLDLSFGC 145
Db 142 TEVVALSRLOGLQSLQDMLWQLDLSFGC 167

RESULT 8
Q6T8R8_BUBBU

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ID QCT888_BUBBU PRELIMINARY; PRT; 146 AA.
AC QCT888;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Leptin (fragment).
OS Bubalus bubalis (Domestic water buffalo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bubalus.
OX NCBI_TaxID=89462;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Adipose tissue;
RA Rajendran S., Shukla D.C., Saravanan B.C.;
RT "Cloning and sequencing of buffalo leptin gene.";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY427959; AK05862.1; -; mRNA.
DR HSSP; P41159; 1AX8.
DR SMR; Q678R8; 3-146.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000065; Leptin.
DR Pfam; PF02024; Leptin; 1.
DR PRINTS; PR00495; LEPTIN.
DR ProDom; PD005698; Leptin; 1.
FT CHAIN <1 146 leptin.
FT NON_TER 1
SQ SEQUENCE 146 AA; 16069 MW; 1A745EE0851BD8CA CRC64;

Query Match 83.8%; Score 612.5; DB 2; Length 146;
Best Local Similarity 86.3%; Pred. No. 1.7e-48;
Matches 126; Conservative 10; Mismatches 9; Indels 1; Gaps 1;

QY 1 VPIQKVDPTKLIKTIIVTRINDISHT-SVSSKQKVTGLDFPGLHPILTSLKMDQTLAV 59
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 VPRIKVDPTKLIKTIIVTRINDISHTQSVSSKQKVTGLDFPGLHPILTSLKMDQTLAI 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 60 YQOILTSMSRNVIOISNDLENRLDLHLVAFKSCHLPHWASGLETLDSLGGVLEASGVY 119
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 YQOILTSLSRNVVQISNDLENRLDLHLVAFKSCPLPQVRALESLSLGVVLEASLYS 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 120 TEVVALSRQGSQDMLWLQDLSPGC 145
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 TEVVALSRQGSQDMLRQLDLSPGC 146
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
OB BOVIN STANDARD; PRT; 167 AA.
AC P50595; Q97918; Q95133; Q9TS29;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Leptin precursor (Obesity factor).
GN Name=LEP; Synonyms=OB, OBS;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RA Tellam R.L., Briscoe S., Vuocolo A.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE OF 22-167.
RA Ji S., Spurlock M.B.;
RT "Partial cloning of bovine obesity gene.";
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RN [3]

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RL Anim. Genet. 27:275-278(1996).
 CC -1- FUNCTION: May function as part of a signaling pathway that acts to
 CC regulate the size of the body fat depot. An increase in the level
 CC of LEP may act directly or indirectly on the CNS to inhibit food
 CC intake and/or regulate energy expenditure as part of a homeostatic
 CC mechanism to maintain constancy of the adipose mass.
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -1- SIMILARITY: Belongs to the leptin family.
 CC -----
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 CC -----
 DR EMBL; U63540; AAB05923.1; -; mRNA.
 DR EMBL; U59894; AAB03458.1; -; mRNA.
 DR EMBL; AF026976; AAB82724.1; -; mRNA.
 DR EMBL; U66254; AAB97308.1; -; Genomic_DNA.
 DR EMBL; AF052691; AAC06303.1; -; mRNA.
 DR EMBL; AF102856; AAC78147.1; -; mRNA.
 DR EMBL; AF477387; AAL84792.1; -; mRNA.
 DR EMBL; AF477386; AAL84792.1; JOINED; Genomic_DNA.
 DR EMBL; U40812; AAC48641.1; -; mRNA.
 DR HSSP; P41159; 1AX8.
 DR SMR; Q29406; 24-167.
 DR InterPro; IPR012351; Cytokine_4_hlx.
 DR InterPro; IPR000065; Leptin.
 DR PANTHER; PTHR11724; Leptin; 1.
 DR Pfam; PF02024; Leptin; 1.
 DR PRINTS; PR00495; LEPTIN.
 DR ProDom; PD005698; Leptin; 1.
 KW Obesity; Signal.
 FT SIGNAL 1 21 Potential.
 FT CHAIN 22 167 Leptin.
 FT DISULFID 117 167 By similarity.
 FT CONFLICT 21 22 AV -> GP (in Ref. 8).
 FT CONFLICT 97 97 I -> L (in Ref. 8).
 FT CONFLICT 122 122 A -> R (in Ref. 4).
 SQ SEQUENCE 167 AA; 18661 MW; 27550E1E0E63814E CRC64;
 Query Match 83.7%; Score 611.5; DB 1; Length 167;
 Best Local Similarity 86.3%; Pred. No. 2.4e-48;
 Matches 126; Conservative 10; Mismatches 9; Indels 1; Gaps 1;
 QY 1 VPIQKVDQDTKLIKTIIVTRINDISH-TSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 59
 DB 22 VPIWRVQDDTKLIKTIIVTRINDISHMQSVSSKQKVTGLDFIPGLHPVLSLSKMDQTLAI 81
 QY 60 YQOILTSMPERNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYS 119
 DB 82 YQOILTSMPERNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYS 141
 QY 120 TEVVALSRQGLQDMLWQLDLSGPC 145
 DB 142 TEVVALSRQGLQDMLWQLDLSGPC 167
 Query Match 83.7%; Score 611.5; DB 1; Length 167;
 Best Local Similarity 86.3%; Pred. No. 2.4e-48;
 Matches 126; Conservative 10; Mismatches 9; Indels 1; Gaps 1;
 QY 1 VPIQKVDQDTKLIKTIIVTRINDISH-TSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 59
 DB 22 VPIWRVQDDTKLIKTIIVTRINDISHMQSVSSKQKVTGLDFIPGLHPVLSLSKMDQTLAI 81
 QY 60 YQOILTSMPERNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYS 119
 DB 82 YQOILTSMPERNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYS 141
 QY 120 TEVVALSRQGLQDMLWQLDLSGPC 145
 DB 142 TEVVALSRQGLQDMLWQLDLSGPC 167
 RESULT 12
 ID Q5TIL9_PIG PRELIMINARY; PRT; 167 AA.
 AC Q5TIL9_PIG
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DE Leptin precursor.
 GN Names=LEP;
 OS Sus scrofa domestica (domestic pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 OC Sus.
 OX NCBI_TaxID=9825;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RA D'Andrea M., Pilla F., Archibald A.L.;
 RT "Structural and expression analysis of Leptin and Melanocortin-4
 receptor genes in Caerfana swine breed.";
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ865080; CA123842.1; -; Genomic_DNA.
 DR SMR; Q5TIL9; 24-167.
 DR GO; GO:0005576; C:extracellular region; IEA.
 DR GO; GO:0005179; P:hormone activity; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR000065; Leptin.
 DR Pfam; PF02024; Leptin; 1.
 DR PRINTS; PR00495; LEPTIN.
 DR ProDom; PD005698; Leptin; 1.
 KW Signal.
 FT SIGNAL 1 21 Potential.
 FT CHAIN 22 167 Leptin.
 SQ SEQUENCE 167 AA; 18661 MW; 27550E1E0E63814E CRC64;
 Query Match 83.7%; Score 611.5; DB 2; Length 167;
 Best Local Similarity 86.3%; Pred. No. 2.4e-48;
 Matches 126; Conservative 10; Mismatches 9; Indels 1; Gaps 1;
 QY 1 VPIQKVDQDTKLIKTIIVTRINDISH-TSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 59
 DB 22 VPIWRVQDDTKLIKTIIVTRINDISHMQSVSSKQKVTGLDFIPGLHPVLSLSKMDQTLAI 81
 QY 60 YQOILTSMPERNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYS 119
 DB 82 YQOILTSMPERNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYS 141
 QY 120 TEVVALSRQGLQDMLWQLDLSGPC 145
 DB 142 TEVVALSRQGLQDMLWQLDLSGPC 167
 RESULT 13
 ID OB_SHEEP STANDARD; PRT; 146 AA.
 AC Q28603; P79212;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Leptin (Obesity factor).
 GN Name=LEP; Synonyms=OB;
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RS TISSUE=Adipose tissue;
 RA Simmons J.M., Dyer C.J., Keisler D.H.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE OF 9-125.
 RC TISSUE=Adipose tissue;
 RX MEDLINE=98006799; PubMed=9347250; DOI=10.1016/S0739-7240(97)00028-3;
 RA Dyer C.J., Simmons J.M., Matteri R.L., Keisler D.H.;
 RT "CDNA cloning and tissue-specific gene expression of ovine leptin,
 RL NPY-Y1 receptor, and NPY-Y2 receptor.";
 RL Domest. Anim. Endocrinol. 14:295-303(1997).
 CC -1- FUNCTION: May function as part of a signaling pathway that acts to
 CC regulate the size of the body fat depot. An increase in the level
 CC of LEP may act directly or indirectly on the CNS to inhibit food
 CC intake and/or regulate energy expenditure as part of a homeostatic
 CC mechanism to maintain constancy of the adipose mass.
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -1- SIMILARITY: Belongs to the leptin family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC -----
DR EMBL; U84247; ABA41786.1; -; mRNA.
DR EMBL; U62123; AAB51033.1; -; mRNA.
DR HSSP; P41159; IAX8.
DR SMR; Q28603; 3-146.
DR InterPro; IPR012351; Cytokine_4_hlx.
DR PANTHER; PTHR11724; Leptin; 1.
DR Pfam; PF02024; Leptin; 1.
DR PRINTS; PR00495; Leptin.
DR ProDom; PD005698; Leptin; 1.
KW Obesity.
FT DISULFID 96 146 By similarity.
FT CONFLICT 65 65 L -> H (in Ref. 2).
FT CONFLICT 92 92 A -> G (in Ref. 2).
FT CONFLICT 124 124 V -> L (in Ref. 2).
SQ SEQUENCE 146 AA; 16054 MW; 19D54C53240968CA CRC64;

Query Match 83.2%; Score 608.5; DB 1; Length 146;
Best Local Similarity 86.3%; Pred. No. 3.9e-48;
Matches 126; Conservative 9; Mismatches 10; Indels 1; Gaps 1;

Qy 1 VPIQKVDQDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTSLKMDQTLAV 59
Db 1 VPIKQVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTSLKMDQTLAI 60
Qy 60 YQOILTSMPNRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDLSLGVLEASGYS 119
Db 61 YQOILASLPNRNVIQISNDLENLRLDLHLVAFSKSCHLPQVRALESLSLGVLEASLYS 120
Qy 120 TEVALSRLOGSLQDMLWQDLSPGC 145
Db 121 TEVALSRLOGSLQDMLRQLDLSPEC 146

RESULT 14

Q5EAE4_BOVIN PRELIMINARY; PRT; 167 AA.
ID Q5EAE4_BOVIN
AC Q5EAE4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Leptin.
GN Name=LEP;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pooled;
RX MEDLINE=21180013; PubMed=11282978; DOI=10.1101/gr.170101;
RA Smith T.P.L., Grosse W.M., Ersking B.A., Roberts A.J., Stone R.T.,
RA Casas E., Wray J.E., White J., Cho J., Fahrenkrug S.C., Bennett G.L.,
RA Heaton M.P., Laegreid W.W., Rohrer G.A., Chitko-Mckown C.G.,
RA Pertea G., Holt I., Karamycheva S., Liang F., Quackenbush J.,
RA Keele J.W.;
RT "Sequence evaluation of four pooled-tissue normalized bovine cDNA
RT libraries and construction of a gene index for cattle.";
RL Genome Res. 11:626-630(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pooled;
RA Harhay G.P., Sonstegard T.S., Clawson M.L., Heaton M.P., Keele J.W.,
RA Snelling W.M., Weidmann R.T., Smith T.P.L.;
RT "Sequencing and analysis of Bos taurus full-length insert cDNA
RT clones.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
RL EMBL; BT020625; AAX08642.1; -; mRNA.

DR SMR; Q5EAE4; 24-167.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000065; Leptin.
DR Pfam; PF02024; Leptin; 1.
DR PRINTS; PR00495; LEPTIN.
SQ SEQUENCE 167 AA; 18663 MW; C9AA16B31AF229CE CRC64;

Query Match 83.2%; Score 608.5; DB 2; Length 167;
Best Local Similarity 86.3%; Pred. No. 4.6e-48;
Matches 126; Conservative 9; Mismatches 10; Indels 1; Gaps 1;

Qy 1 VPIQKVDQDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTSLKMDQTLAV 59
Db 22 VPIKQVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTSLKMDQTLAI 81
Qy 60 YQOILTSMPNRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDLSLGVLEASGYS 119
Db 82 YQOILTSLPNRNVIQISNDLENLRLDLHLVAFSKSCHLPQVRALESLSLGVLEASLYS 141
Qy 120 TEVALSRLOGSLQDMLWQDLSPGC 145
Db 142 TEVALSRLOGSLQDMLRQLDLSPEC 167

RESULT 15

Q4VW71_CTEID PRELIMINARY; PRT; 146 AA.
ID Q4VW71_CTEID
AC Q4VW71;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Obese protein (fragment).
OS Ctenopharyngodon idella (Grass carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Ctenopharyngodon.
OX NCBI_TaxID=7959;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mesenteric adipose tissue;
RA Dai H., Long L.;
RT "Molecular cloning and sequence analysis of the obese gene from the
RT Ctenopharyngodon idellus.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY551335; AAT45394.1; -; mRNA.
FT NON_TER 1
SQ SEQUENCE 146 AA; 16004 MW; 60D1A3BF6EB062AB CRC64;
Query Match 82.6%; Score 603.5; DB 2; Length 146;
Best Local Similarity 84.2%; Pred. No. 1.1e-47;
Matches 123; Conservative 13; Mismatches 9; Indels 1; Gaps 1;

Qy 1 VPIQKVDQDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTSLKMDQTLAV 59
Db 1 VPIKQVDDTKTLIKTIVTRINDISHTQSVSAKQKVTGLDFIPGLHPILTSLKMDQTLAV 60
Qy 60 YQOILTSMPNRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDLSLGVLEASGYS 119
Db 61 YQOVLTSLPNQVLIQISNDLENLRLDLHLVAFSKSCHLPQTSGLQKPSLGSVLEASLYS 120
Qy 120 TEVALSRLOGSLQDMLWQDLSPGC 145
Db 121 TEVALSRLOGSLQDILQDLVSPEC 146

Search completed: May 4, 2006, 21:57:12
Job time : 145.502 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 21:52:45 ; Search time 32.8866 Seconds
(without alignments)
364.525 Million cell updates/sec

Title: US-10-623-189-2
Perfect score: 731
Sequence: 1 VPIQKVQDDTKTLIKTIVTR.....SRLQGSLLQDMLWLDLSPGC 145

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pdp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	731	100.0	166	1 US-08-347-563A-6	Sequence 6, Appli
2	731	100.0	166	2 US-08-292-345B-6	Sequence 6, Appli
3	731	100.0	166	2 US-08-485-942A-6	Sequence 6, Appli
4	731	100.0	166	2 US-08-488-214A-6	Sequence 6, Appli
5	731	100.0	166	2 US-08-488-208A-6	Sequence 6, Appli
6	731	100.0	166	2 US-08-483-211A-6	Sequence 6, Appli
7	731	100.0	166	2 US-08-488-223A-6	Sequence 6, Appli
8	731	100.0	166	2 US-08-438-431A-6	Sequence 6, Appli
9	731	100.0	166	2 US-08-488-225A-6	Sequence 6, Appli
10	731	100.0	166	2 US-09-204-730B-6	Sequence 6, Appli
11	731	100.0	166	2 US-09-316-393-6	Sequence 6, Appli
12	731	100.0	166	2 US-09-686-647A-6	Sequence 6, Appli
13	720.5	98.6	146	1 US-08-398-021-3	Sequence 3, Appli
14	720.5	98.6	146	1 US-08-788-943A-1	Sequence 1, Appli
15	720.5	98.6	146	1 US-08-788-943A-4	Sequence 4, Appli
16	720.5	98.6	146	1 US-08-788-943A-5	Sequence 5, Appli
17	720.5	98.6	146	1 US-08-823-104-3	Sequence 3, Appli
18	720.5	98.6	146	1 US-08-823-104-5	Sequence 5, Appli
19	720.5	98.6	146	1 US-08-804-668-1	Sequence 1, Appli
20	720.5	98.6	146	1 US-09-003-081-6	Sequence 6, Appli
21	720.5	98.6	146	2 US-08-648-262-6	Sequence 6, Appli
22	720.5	98.6	146	2 US-08-648-263-6	Sequence 6, Appli
23	720.5	98.6	146	2 US-08-674-774-4	Sequence 4, Appli
24	720.5	98.6	146	2 US-08-914-375C-32	Sequence 32, Appli
25	720.5	98.6	146	2 US-09-172-644-1	Sequence 1, Appli
26	720.5	98.6	146	2 US-09-221-178-1	Sequence 1, Appli
27	720.5	98.6	146	2 US-09-200-919-1	Sequence 1, Appli

28	720.5	98.6	146	4 PCT-US96-00952-2	Sequence 2, Appli
29	720.5	98.6	146	4 PCT-US96-00952-3	Sequence 3, Appli
30	720.5	98.6	147	2 US-09-200-919-4	Sequence 4, Appli
31	720.5	98.6	148	1 US-08-429-362-3	Sequence 3, Appli
32	720.5	98.6	148	1 US-08-823-104-18	Sequence 18, Appli
33	720.5	98.6	167	1 US-08-540-242A-4	Sequence 4, Appli
34	720.5	98.6	167	1 US-08-347-563A-4	Sequence 4, Appli
35	720.5	98.6	167	1 US-09-003-081-5	Sequence 5, Appli
36	720.5	98.6	167	2 US-08-292-345B-4	Sequence 4, Appli
37	720.5	98.6	167	2 US-08-648-262-5	Sequence 5, Appli
38	720.5	98.6	167	2 US-08-648-263-5	Sequence 5, Appli
39	720.5	98.6	167	2 US-08-485-942A-4	Sequence 4, Appli
40	720.5	98.6	167	2 US-08-488-214A-4	Sequence 4, Appli
41	720.5	98.6	167	2 US-08-488-208A-4	Sequence 4, Appli
42	720.5	98.6	167	2 US-08-759-628-1	Sequence 1, Appli
43	720.5	98.6	167	2 US-08-688-908-7	Sequence 7, Appli
44	720.5	98.6	167	2 US-08-483-211A-4	Sequence 4, Appli
45	720.5	98.6	167	2 US-08-488-223A-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-347-563A-6
; Sequence 6, Application US/08347563A
; Patent No. 5935810
; GENERAL INFORMATION:
; APPLICANT: THE ROCKEFELLER UNIVERSITY
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC
; TITLE OF INVENTION: ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THERE-
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/347,563A
; FILING DATE: No. 5935810ember 30, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Human ob polypeptide lacking Gln at position 49
; ORIGINAL SOURCE:
; ORGANISM: Human
; US-08-347-563A-6

Query Match 100.0%; Score 731; DB 1; Length 166;
Best Local Similarity 100.0%; Pred. No. 1e-73;

Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAVY 60
Db 22 VPIQKVDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAVY 81
Qy 61 QQLTSMPSNRVQISNDLENRLDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYST 120
Db 82 QQLTSMPSNRVQISNDLENRLDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYST 141
Qy 121 EVVALSRQSGSLQDMLWQLDLSGPC 145
Db 142 EVVALSRQSGSLQDMLWQLDLSGPC 166

RESULT 2

US-08-292-345B-6
; Sequence 6, Application US/08292345B
; Patent No. 6001968
; GENERAL INFORMATION:
; APPLICANT: THE ROCKEFELLER UNIVERSITY
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC
; ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,345B
; FILING DATE: August 17, 1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Ob protein harboring Gln deletion at position 49
; ORIGINAL SOURCE:
; ORGANISM: Human
; US-08-292-345B-6

Query Match 100.0%; Score 731; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAVY 60
Db 22 VPIQKVDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAVY 81
Qy 61 QQLTSMPSNRVQISNDLENRLDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYST 120
Db 82 QQLTSMPSNRVQISNDLENRLDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYST 141
Qy 121 EVVALSRQSGSLQDMLWQLDLSGPC 145

Db 142 EVVALSRQSGSLQDMLWQLDLSGPC 166

RESULT 3

US-08-485-942A-6
; Sequence 6, Application US/08485942A
; Patent No. 6048837
; GENERAL INFORMATION:
; APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA,
; MARGHERITA MAFFEI, JEFFREY HALAAS, KETAN GAJIWALA, AND STEPHEN K. BURL
; TITLE OF INVENTION: OB POLYPEPTIDE AS MODULATORS OF BODY WEIGHT (AS
; AMENDED)
; NUMBER OF SEQUENCES: 99
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,942A
; FILING DATE: JUNE 7, 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/438,431
; FILING DATE: May 10, 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/347,563
; FILING DATE: No. 6048837ember 30, 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP 2F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Human ob polypeptide lacking Gln at position
; DESCRIPTION: 49
; ORIGINAL SOURCE:
; ORGANISM: Human
; US-08-485-942A-6

Query Match 100.0%; Score 731; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAVY 60
Db 22 VPIQKVDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAVY 81
Qy 61 QQLTSMPSNRVQISNDLENRLDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYST 120
Db 82 QQLTSMPSNRVQISNDLENRLDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYST 141

QY 121 EVVALSRLOGSLQDMLWQLDLSFGC 145
|
Db 142 EVVALSRLOGSLQDMLWQLDLSFGC 166
|

RESULT 4

US-08-488-214A-6
; Sequence 6, Application US/08488214A
; Patent No. 6124439
; GENERAL INFORMATION:
; APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA,
; APPLICANT: MARGHERITA MARFEEI, JEFFREY HALAAS, KETAN GAJIWALA, AND STEPHEN K. BURL
; TITLE OF INVENTION: OB POLYPEPTIDE ANTIBODIES AND METHOD OF MAKING
; TITLE OF INVENTION: (AS AMENDED)
; NUMBER OF SEQUENCES: 99
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,214A
; FILING DATE: JUNE 7, 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/438,431
; FILING DATE: May 10, 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/347,563
; FILING DATE: No. 6124439ember 30, 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP 2D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Human ob polypeptide lacking Gln at position
; ORIGINAL SOURCE:
; ORGANISM: Human
; US-08-488-214A-6

Query Match 100.0%; Score 731; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPIQKQVDDTKLIKTIIVTRINDISHTSVSSKQKVTGLDFIPGLPIILTLSSKQDQTLAVY 60
|
Db 22 VPIQKQVDDTKLIKTIIVTRINDISHTSVSSKQKVTGLDFIPGLPIILTLSSKQDQTLAVY 81
|
QY 61 QQILTSMPSRNVIOISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYST 120
|

Db 82 QQILTSMPSRNVIOISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYST 141
|
QY 121 EVVALSRLOGSLQDMLWQLDLSFGC 145
|
Db 142 EVVALSRLOGSLQDMLWQLDLSFGC 166
|

RESULT 5

US-08-488-208A-6
; Sequence 6, Application US/08488208A
; Patent No. 6124448
; GENERAL INFORMATION:
; APPLICANT: THE ROCKEFELLER UNIVERSITY
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,208A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/485,943
; FILING DATE: June 7, 1995
; APPLICATION NUMBER: 08/438,431
; FILING DATE: May 10, 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/347,563
; FILING DATE: No. 6124448ember 30, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP2I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Human ob polypeptide lacking Gln at position 49
; ORIGINAL SOURCE:
; ORGANISM: Human
; US-08-488-208A-6

Query Match 100.0%; Score 731; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPIQKQVDDTKLIKTIIVTRINDISHTSVSSKQKVTGLDFIPGLPIILTLSSKQDQTLAVY 60
|
Db 22 VPIQKQVDDTKLIKTIIVTRINDISHTSVSSKQKVTGLDFIPGLPIILTLSSKQDQTLAVY 81
|

Qy 61 QQILTSPSRNVQISNDLENRLDLHLVLAFSKSHLPWASGLETLDSLGVLASGYST 120
Db 82 QQILTSPSRNVQISNDLENRLDLHLVLAFSKSHLPWASGLETLDSLGVLASGYST 141
Qy 121 EVVALSRLOGSLQDMLWQLDLSFGC 145
Db 142 EVVALSRLOGSLQDMLWQLDLSFGC 166

RESULT 6
US-08-483-211A-6
; Sequence 6, Application US/08483211A
; Patent No. 6309853
; GENERAL INFORMATION:
; APPLICANT: THE ROCKEFELLER UNIVERSITY
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS: 98
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,211A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/485,943
; FILING DATE: June 7, 1995
; APPLICATION NUMBER: 08/438,431
; FILING DATE: May 10, 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/347,563
; FILING DATE: No. 6309853ember 30, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP21
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Human ob polypeptide lacking Gln at position 49
; ORIGINAL SOURCE:
; ORGANISM: Human
US-08-483-211A-6

Query Match 100.0%; Score 731; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKKQVGTGLDFIPGLHPILTLSKMDQTLAVY 60
Db 22 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKKQVGTGLDFIPGLHPILTLSKMDQTLAVY 81
Qy 61 QQILTSPSRNVQISNDLENRLDLHLVLAFSKSHLPWASGLETLDSLGVLASGYST 120
Db 82 QQILTSPSRNVQISNDLENRLDLHLVLAFSKSHLPWASGLETLDSLGVLASGYST 141
Qy 121 EVVALSRLOGSLQDMLWQLDLSFGC 145
Db 142 EVVALSRLOGSLQDMLWQLDLSFGC 166

RESULT 7
US-08-488-223A-6
; Sequence 6, Application US/08488223A
; Patent No. 6350730
; GENERAL INFORMATION:
; APPLICANT: THE ROCKEFELLER UNIVERSITY
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC
; TITLE OF INVENTION: ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES TH
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,223A
; FILING DATE: 07-Jun-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/485,943
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/347,563
; FILING DATE: No. 6350730ember 30, 1994
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Human ob polypeptide lacking Gln at position 49
; ORIGINAL SOURCE:
; ORGANISM: Human
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-488-223A-6

Query Match 100.0%; Score 731; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKKQVGTGLDFIPGLHPILTLSKMDQTLAVY 60
Db 22 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKKQVGTGLDFIPGLHPILTLSKMDQTLAVY 81

Qy	61	QOII	TSPSRNVI	QISDN	ENLRD	LLH	LA	FSK	CHL	PWAS	GLET	DS	LG	VLEAS	GYST	120
Db	82	QOII	TSPSRNVI	QISDN	ENLRD	LLH	LA	FSK	CHL	PWAS	GLET	DS	LG	VLEAS	GYST	141
Qy	121	EWAL	SRLQ	SLQD	MLW	QD	LS	PGC	145							
Db	142	EWAL	SRLQ	SLQD	MLW	QD	LS	PGC	166							

RESULT 8
 US-08-438-431A-6
 Sequence 6, Application US/08438431A
 Patent No. 6429290
 GENERAL INFORMATION:
 APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA, MARGHERITA MAFFEI,
 TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC ACIDS AND PR
 NUMBER OF SEQUENCES: 99
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Klauber & Jackson
 STREET: 411 Hackensack Avenue
 CITY: Hackensack
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/438,431A
 FILING DATE: May 10, 1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/347,563
 FILING DATE: No. 6429290ember 30, 1994
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/292,345
 FILING DATE: August 17, 1994
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 600-1-087 CIPI
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201 487-5800
 TELEFAX: 201 343-1684
 TELEX: 133521
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 166 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 DESCRIPTION: Human ob polypeptide lacking Gln at position 49
 ORIGINAL SOURCE:
 ORGANISM: Human
 US-08-438-431A-6

Db 142 EVVALSRQGSQDMLWQDLSPGC 166

RESULT 9

US-08-488-225A-6

Sequence 6, Application US/08488225A

Patent No. 6471956

GENERAL INFORMATION:

APPLICANT: THE ROCKEFELLER UNIVERSITY

TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING

TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS, AND DIAGNOST

NUMBER OF SEQUENCES: 98

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson

STREET: 411 Hackensack Avenue

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/488,225A

FILING DATE: June 7, 1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/483,211

FILING DATE: June 7, 1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/347,563

FILING DATE: No. 6471956member 30, 1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/292,345

FILING DATE: August 17, 1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-087 CIP2J

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

TELEFAX: 201 343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 166 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

DESCRIPTION: Human ob polypeptide lacking Gln at position

DISCRPTION: 49

ORIGINAL SOURCE:

ORGANISM: Human

US-08-488-225A-6

QY 61 QQILTSMPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLTLDLSLGGVLEASGYST 120
Db 82 QQILTSMPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLTLDLSLGGVLEASGYST 141
QY 121 EVVALSRLOGLQDMLWQLDLSGPC 145
Db 142 EVVALSRLOGLQDMLWQLDLSGPC 166

RESULT 10
US-09-204-730B-6
; Sequence 6, Application US/09204730B
; Patent No. 6703493
; GENERAL INFORMATION:
; APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA
; TITLE OF INVENTION: OB POLYPEPTIDE ANTIBODIES AND METHOD OF MAKING
; (AS AMENDED)
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/204,730B
; FILING DATE: 03-Dec-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521

INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Human ob polypeptide lacking Gln at position
; ORIGINAL SOURCE:
; ORGANISM: Human
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-204-730B-6

Query Match 100.0%; Score 731; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPIQKVDDTKTLIKTIVTRINDISHTSVSSKKQVTGLDFIPGLHPILTILSKMDQTLAVY 60
Db 22 VPIQKVDDTKTLIKTIVTRINDISHTSVSSKKQVTGLDFIPGLHPILTILSKMDQTLAVY 81

QY 61 QQILTSMPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLTLDLSLGGVLEASGYST 120
Db 82 QQILTSMPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLTLDLSLGGVLEASGYST 141
QY 121 EVVALSRLOGLQDMLWQLDLSGPC 145
Db 142 EVVALSRLOGLQDMLWQLDLSGPC 166

RESULT 11
US-09-316-393-6
; Sequence 6, Application US/09316393
; Patent No. 6734160
; GENERAL INFORMATION:
; APPLICANT: THE ROCKEFELLER UNIVERSITY
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC
; ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THERE
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/316,393
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521

INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Ob protein harboring Gln deletion at position 49
; ORIGINAL SOURCE:
; ORGANISM: Human
; US-09-316-393-6

Query Match 100.0%; Score 731; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPIQKVDDTKTLIKTIVTRINDISHTSVSSKKQVTGLDFIPGLHPILTILSKMDQTLAVY 60
Db 22 VPIQKVDDTKTLIKTIVTRINDISHTSVSSKKQVTGLDFIPGLHPILTILSKMDQTLAVY 81

QY 61 QQILTSMPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLTLDLSLGGVLEASGYST 120
Db 82 QQILTSMPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLTLDLSLGGVLEASGYST 141
QY 121 EVVALSRLOGLQDMLWQLDLSGPC 145
Db 142 EVVALSRLOGLQDMLWQLDLSGPC 166

RESULT 12
US-09-686-647A-6
; Sequence 6, Application US/09686647A
; Patent No. 6821945
; GENERAL INFORMATION:
; APPLICANT: The Rockefeller University
; APPLICANT: Jeffrey M. Friedman
; APPLICANT: Yiyang Zhang

APPLICANT: Ricardo Proenca
APPLICANT: Margherita Maffei
APPLICANT: Jeffrey L. Halaas
APPLICANT: Ketan Gajiwala
APPLICANT: Stephen K. Burley
TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 600-1-087/CIPDIVCON
CURRENT APPLICATION NUMBER: US/09/686,647A
CURRENT FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: 09/183,374
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 08/347,563
PRIOR FILING DATE: 1994-11-30
PRIOR APPLICATION NUMBER: 08/292,345
PRIOR FILING DATE: 1994-08-17
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 166
TYPE: PRT
ORGANISM: Homo sapiens
US-09-686-647A-6

Query Match 100.0%; Score 731; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPIQKVDDTKTIKTIIVTRINDISHTSVSSKQKVTGLDFIPGLHPIILTSKMDQTLAVY 60
Db 22 VPIQKVDDTKTIKTIIVTRINDISHTSVSSKQKVTGLDFIPGLHPIILTSKMDQTLAVY 81
Qy 61 QQILTSPSRNVIQISNDLENLRLDLHLVLAFAFKSCHLPWASGLETLDSLGVLASGYST 120
Db 82 QQILTSPSRNVIQISNDLENLRLDLHLVLAFAFKSCHLPWASGLETLDSLGVLASGYST 141
Qy 121 EVVALSRLOGLQDMLWQLDLSGPC 145
Db 142 EVVALSRLOGLQDMLWQLDLSGPC 166

RESULT 13
US-08-398-021-3
Sequence 3, Application US/08398021
Patent No. 5594101
GENERAL INFORMATION:
APPLICANT: Becker, Gerald W.
APPLICANT: Hale, John E.
APPLICANT: Mackellar 1, Warren C.
TITLE OF INVENTION: ANTI-OBESITY PROTEINS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center/Patent Division
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,021
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Caltrider, Steven P.
REGISTRATION NUMBER: 36,467
REFERENCE/DOCKET NUMBER: X10001
TELECOMMUNICATION INFORMATION:

TELEPHONE: 317-276-0757
TELEFAX: 317-277-1917
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-398-021-3

Query Match 98.6%; Score 720.5; DB 1; Length 146;
Best Local Similarity 99.3%; Pred. No. 1.2e-72;
Matches 145; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 VPIQKVDDTKTIKTIIVTRINDISHTSVSSKQKVTGLDFIPGLHPIILTSKMDQTLAV 59
Db 1 VPIQKVDDTKTIKTIIVTRINDISHTSVSSKQKVTGLDFIPGLHPIILTSKMDQTLAV 60
Qy 60 YQILTSPSRNVIQISNDLENLRLDLHLVLAFAFKSCHLPWASGLETLDSLGVLASGYST 119
Db 61 YQILTSPSRNVIQISNDLENLRLDLHLVLAFAFKSCHLPWASGLETLDSLGVLASGYST 120
Qy 120 TEVVALSRLOGLQDMLWQLDLSGPC 145
Db 121 TEVVALSRLOGLQDMLWQLDLSGPC 146

RESULT 14
US-08-788-943A-1
Sequence 1, Application US/08788943A
Patent No. 5831017
GENERAL INFORMATION:
APPLICANT: Hoffmann, James Arthur
TITLE OF INVENTION: OBESITY PROTEIN ANALOG COMPOUNDS AND
TITLE OF INVENTION: FORMULATIONS THEREOF
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center/Patent Division
CITY: Indianapolis
STATE: Indiana
COUNTRY: USA
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,943A
FILING DATE: 24-JAN-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Caltrider, Steven P.
REGISTRATION NUMBER: 36,467
REFERENCE/DOCKET NUMBER: X10540
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0757
TELEFAX: (317) 277-1917
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Modified-site
LOCATION: 28
OTHER INFORMATION: /note="Xaa at position 28 is Gln
OTHER INFORMATION: or absent;"
US-08-788-943A-1

Query Match 98.6%; Score 720.5; DB 1; Length 146;
Best Local Similarity 99.3%; Pred. No. 1.2e-72;
Matches 145; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 VPIQKVDDTKLIKTIIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 59
Db 1 VPIQKVDDTKLIKTIIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 60
Qy 60 YQQLTSMPSRNVIIQISNDLENLRLDLHLVLAFAKSKCHLPWASGLETLDSIGGVLEASGYS 119
Db 61 YQQLTSMPSRNVIIQISNDLENLRLDLHLVLAFAKSKCHLPWASGLETLDSIGGVLEASGYS 120
Qy 120 TEVVALSRLOQSLQDMLWQLDLSPGC 145
Db 121 TEVVALSRLOQSLQDMLWQLDLSPGC 146

RESULT 15
US-08-788-943A-4
; Sequence 4, Application US/08788943A
; Patent No. 5831017
; GENERAL INFORMATION:
; APPLICANT: Hoffmann, James Arthur
; TITLE OF INVENTION: OBESITY PROTEIN ANALOG COMPOUNDS AND
; TITLE OF INVENTION: FORMULATIONS THEREOF
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center/Patent Division
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/788,943A
; APPLICATION NUMBER: US/08/788,943A
; FILING DATE: 24-JAN-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Caltrider, Steven P
; REGISTRATION NUMBER: 36,467
; REFERENCE/DOCKET NUMBER: X10540
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0757
; TELEFAX: (317) 277-1917
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 28
; OTHER INFORMATION: /note= "xaa at position 28 is Gln
; OTHER INFORMATION: or absent,"
US-08-788-943A-4

Query Match 98.6%; Score 720.5; DB 1; Length 146;
Best Local Similarity 99.3%; Pred. No. 1.2e-72;
Matches 145; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 VPIQKVDDTKLIKTIIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 59
Db 1 VPIQKVDDTKLIKTIIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 60
Qy 60 YQQLTSMPSRNVIIQISNDLENLRLDLHLVLAFAKSKCHLPWASGLETLDSIGGVLEASGYS 119

Db 61 YQQLTSMPSRNVIIQISNDLENLRLDLHLVLAFAKSKCHLPWASGLETLDSIGGVLEASGYS 120
Qy 120 TEVVALSRLOQSLQDMLWQLDLSPGC 145
Db 121 TEVVALSRLOQSLQDMLWQLDLSPGC 146
Search completed: May 4, 2006, 21:58:24
Job time : 32.8866 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 4, 2006, 21:57:29 ; Search time 112.113 seconds
(without alignments)
540.393 Million cell updates/sec

Title: US-10-623-189-2
Perfect score: 731
Sequence: 1 VPIQKQDDTKTKTIKTIVTR.....SRQGSLQDMLWQLDLSPGC 145

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues
Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	731	100.0	145	5	US-10-623-189-2	Sequence 2, Appli
2	731	100.0	166	3	US-09-736-084-6	Sequence 6, Appli
3	731	100.0	166	3	US-09-316-393-6	Sequence 6, Appli
4	731	100.0	166	4	US-10-730-488-6	Sequence 6, Appli
5	731	100.0	166	4	US-10-780-295-6	Sequence 6, Appli
6	720.5	98.6	146	4	US-10-191-377-1	Sequence 1, Appli
7	720.5	98.6	146	4	US-10-139-794-10	Sequence 10, Appli
8	720.5	98.6	146	4	US-10-419-058-2	Sequence 2, Appli
9	720.5	98.6	146	4	US-10-467-114-1	Sequence 1, Appli
10	720.5	98.6	146	4	US-10-622-998-1	Sequence 1, Appli
11	720.5	98.6	146	4	US-10-658-834A-211	Sequence 211, App
12	720.5	98.6	146	4	US-10-468-496-1	Sequence 1, Appli
13	720.5	98.6	146	5	US-10-872-198-127	Sequence 127, App
14	720.5	98.6	146	5	US-10-623-189-1	Sequence 1, Appli
15	720.5	98.6	146	5	US-10-502-344-22	Sequence 22, Appli
16	720.5	98.6	146	6	US-11-021-951-127	Sequence 127, App
17	720.5	98.6	167	3	US-09-736-084-4	Sequence 4, Appli
18	720.5	98.6	167	3	US-09-928-522-7	Sequence 7, Appli
19	720.5	98.6	167	3	US-09-789-306-3	Sequence 3, Appli
20	720.5	98.6	167	3	US-09-804-409A-11	Sequence 11, Appli
21	720.5	98.6	167	3	US-09-316-393-4	Sequence 4, Appli
22	720.5	98.6	167	4	US-10-440-454-67	Sequence 67, Appli
23	720.5	98.6	167	4	US-10-458-334-17	Sequence 17, Appli
24	720.5	98.6	167	4	US-10-730-488-4	Sequence 4, Appli
25	720.5	98.6	167	4	US-10-780-295-4	Sequence 4, Appli
26	720.5	98.6	167	5	US-10-723-860-2482	Sequence 2482, Ap
27	720.5	98.6	167	5	US-10-698-510-17	Sequence 17, Appli

28	720.5	98.6	167	5	US-10-775-180-168	Sequence 168, App
29	720.5	98.6	167	5	US-10-775-180-169	Sequence 169, App
30	720.5	98.6	167	5	US-10-775-180-170	Sequence 170, App
31	720.5	98.6	167	5	US-10-775-180-171	Sequence 171, App
32	720.5	98.6	167	5	US-10-893-315-63	Sequence 63, Appli
33	720.5	98.6	167	5	US-10-756-149-5381	Sequence 5381, Ap
34	720.5	98.6	167	5	US-10-775-204-551	Sequence 551, App
35	720.5	98.6	167	5	US-10-775-204-555	Sequence 555, App
36	720.5	98.6	167	5	US-10-775-204-557	Sequence 557, App
37	720.5	98.6	167	5	US-10-775-204-558	Sequence 558, App
38	720.5	98.6	167	6	US-11-060-291-1	Sequence 1, Appli
39	720.5	98.6	171	5	US-10-908-400A-105	Sequence 105, App
40	720.5	98.6	178	5	US-10-893-315-108	Sequence 108, App
41	720.5	98.6	374	4	US-10-679-999-15	Sequence 15, Appli
42	720.5	98.6	374	4	US-10-679-999-18	Sequence 18, Appli
43	720.5	98.6	374	6	US-11-054-085-15	Sequence 15, Appli
44	720.5	98.6	374	6	US-11-054-085-18	Sequence 18, Appli
45	720.5	98.6	379	4	US-10-679-999-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1

US-10-623-189-2
; Sequence 2, Application US/10623189
; Publication No. US20050020496A1
; GENERAL INFORMATION:
; APPLICANT: DEPAOLI, Alex M.
; APPLICANT: ORAL, Elif Arioglu
; APPLICANT: TAYLOR, Simeon I.
; APPLICANT: GARG, Abhimanyu
; TITLE OF INVENTION: USE OF LEPTIN FOR TREATING HUMAN LIPOATROPHY AND METHOD OF DETER
; TITLE OF INVENTION: PREDISPOSITION TO SAID TREATMENT
; FILE REFERENCE: 54113.8005.US02
; CURRENT APPLICATION NUMBER: US/10/623.189
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 10/279,129
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: US 60/336,394
; PRIOR FILING DATE: 2001-10-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant Leptin Human 145 (rHu-Leptin 1-145)
US-10-623-189-2

Query Match	100.0%;	Score 731;	DB 5;	Length 145;
Best Local Similarity	100.0%;	Pred. No. 3.8e-71;		
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Db	1	VPIQKQVDDTKTKTIKTIVTRINDISHTSVSKQKVTGLDPIGLHPILTLTKMDQTLAVY	60	
Qy	61	QQILTSMPSRNVIQISNDLENRLMLVLAFLAPSKSCHLPWASGLETLDSLGGLVLEASGYST	120	
Db	61	QQILTSMPSRNVIQISNDLENRLMLVLAFLAPSKSCHLPWASGLETLDSLGGLVLEASGYST	120	
Qy	121	EWVALSRQGSLODMLWQLDLSPGC	145	
Db	121	EWVALSRQGSLODMLWQLDLSPGC	145	

RESULT 2

US-09-736-084-6
; Sequence 6, Application US/09736084
; Patent No. US20020107211A1
; GENERAL INFORMATION:


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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/730,488
; FILING DATE: 08-Dec-2003
; CLASSIFICATION: <Unknown>
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/736,084
; FILING DATE: 13-Dec-2000
; APPLICATION NUMBER: 08/438,431
; FILING DATE: May 10, 1995
; APPLICATION NUMBER: 08/347,563
; FILING DATE: November 30, 1994
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP 2D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
;
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Human ob polypeptide lacking Gln at position
; ORIGINAL SOURCE:
; ORGANISM: Human
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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; US-10-730-488-6
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; Query Match 100.0%; Score 731; DB 4; Length 166;
; Best Local Similarity 100.0%; Pred. No. 4.6e-71;
; Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Db 22 VPIQKVDDTKTLIKTIIVTRINDISHTSVSSKQKVGTGLDFIPGLHPILTLKMDQTLAVY 81
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; Qy 61 QQILTSPSRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYST 120
; Db 82 QQILTSPSRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYST 141
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; Qy 121 EVVALSRQSGLDMLWQLDLSPGC 145
; Db 142 EVVALSRQSGLDMLWQLDLSPGC 166
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; RESULT 5
; US-10-780-295-6
; Sequence 6, Application US/10780295
; Publication No. US20040214214A1
; GENERAL INFORMATION:
; APPLICANT: THE ROCKEFELLER UNIVERSITY
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC
; ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THE
;
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/780,295
; FILING DATE: 17-Feb-2004
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/316,393
; FILING DATE: 21-May-1999
; APPLICATION NUMBER: 08/292,345
; FILING DATE: 17-August-1994
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
;
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Ob protein harboring Gln deletion at position 49
; ORIGINAL SOURCE:
; ORGANISM: Human
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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; US-10-780-295-6
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; Query Match 100.0%; Score 731; DB 4; Length 166;
; Best Local Similarity 100.0%; Pred. No. 4.6e-71;
; Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Qy 1 VPIQKVDDTKTLIKTIIVTRINDISHTSVSSKQKVGTGLDFIPGLHPILTLKMDQTLAVY 60
; Db 22 VPIQKVDDTKTLIKTIIVTRINDISHTSVSSKQKVGTGLDFIPGLHPILTLKMDQTLAVY 81
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; Qy 61 QQILTSPSRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYST 120
; Db 82 QQILTSPSRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYST 141
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; Qy 121 EVVALSRQSGLDMLWQLDLSPGC 145
; Db 142 EVVALSRQSGLDMLWQLDLSPGC 166
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; RESULT 6
; US-10-191-377-1
; Sequence 1, Application US/10191377
; Publication No. US2003009709A1
; GENERAL INFORMATION:
; APPLICANT: AMGEN INC.
; TITLE OF INVENTION: BIODEGRADABLE, pH/THERMOSENSITIVE HYDROGEL FOR
; SUSTAINED DELIVERY OF BIOLOGICALLY ACTIVE AGENTS
;
; FILE REFERENCE: A-575
; CURRENT APPLICATION NUMBER: US/10/191,377
; CURRENT FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 146
; TYPE: PPT
; ORGANISM: Human Leptin
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; US-10-191-377-1
;
; Query Match 98.6%; Score 720.5; DB 4; Length 146;
; Best Local Similarity 99.3%; Pred. No. 5.3e-70;
; Matches 145; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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; Qy 1 VPIQKVDDTKTLIKTIIVTRINDISHT-SVSSKQKVGTGLDFIPGLHPILTLKMDQTLAV 59

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APPLICANT: Ladd, David
APPLICANT: Papisov, Mikhail
TITLE OF INVENTION: PROTEIN CONJUGATES WITH A WATER-SOLUBLE BIOCOMPATIBLE, BIODEGRADABLE
TITLE OF INVENTION: POLYMER
FILE REFERENCE: A-822
CURRENT APPLICATION NUMBER: US/10/622,998
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 60/397,509
PRIOR FILING DATE: 2002-07-19
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patent in version 3.1
SEQ ID NO 1
LENGTH: 146
TYPE: PRT
ORGANISM: Homo sapiens
US-10-622-998-1

Query Match 98.6%; Score 720.5; DB 4; Length 146;
Best Local Similarity 99.3%; Pred. No. 5.3e-70;
Matches 145; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 VPIQKVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 59
Db 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60

Qy 60 YQQLTSMPSNRVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDLSLGGVLEASGYS 119
Db 61 YQQLTSMPSNRVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDLSLGGVLEASGYS 120

Qy 120 TEVVALSRQSLQDMLWQLDLSGPC 145
Db 121 TEVVALSRQSLQDMLWQLDLSGPC 146

RESULT 11
US-10-658-834A-211
Sequence 211, Application US/10658834A
Publication No. US20040132977A1
GENERAL INFORMATION:
APPLICANT: Gantier, Rene
APPLICANT: Guyon, Thierry
APPLICANT: Dristanti, Lila
APPLICANT: Vega, Manuel
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
TITLE OF INVENTION: Acid
TITLE OF INVENTION: Molecules and Related Applications
FILE REFERENCE: 38751-922
CURRENT APPLICATION NUMBER: US/10/658,834A
CURRENT FILING DATE: 2003-09-08
PRIOR APPLICATION NUMBER: 60/457,135
PRIOR FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: 60/409,898
PRIOR FILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 1306
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 211
LENGTH: 146
TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank AAA60470
DATABASE ENTRY DATE: 1995-01-13
US-10-658-834A-211

Query Match 98.6%; Score 720.5; DB 4; Length 146;
Best Local Similarity 99.3%; Pred. No. 5.3e-70;
Matches 145; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 VPIQKVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 59
Db 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60

Qy 60 YQQLTSMPSNRVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDLSLGGVLEASGYS 119
Db 61 YQQLTSMPSNRVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDLSLGGVLEASGYS 120

Qy 120 TEVVALSRQSLQDMLWQLDLSGPC 145
Db 121 TEVVALSRQSLQDMLWQLDLSGPC 146

RESULT 12
US-10-468-496-1
Sequence 1, Application US/10468496
Publication No. US20040180386A1
GENERAL INFORMATION:
APPLICANT: Carr, Francis J.
APPLICANT: Jones, Tim
APPLICANT: Williams, Stephen
APPLICANT: Hamilton, Anita
TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED
TITLE OF INVENTION: IMMUNOGENICITY
FILE REFERENCE: MER-117
CURRENT APPLICATION NUMBER: US/10/468,496
CURRENT FILING DATE: 2003-09-25
PRIOR APPLICATION NUMBER: 01103954.2
PRIOR FILING DATE: 2001-02-19
PRIOR APPLICATION NUMBER: 01105777.5
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 01106538.0
PRIOR FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 01106536.4
PRIOR FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 01107012.5
PRIOR FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 01106899.6
PRIOR FILING DATE: 2001-03-20
NUMBER OF SEQ ID NOS: 2036
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 146
TYPE: PRT
ORGANISM: Homo sapiens
US-10-468-496-1

Query Match 98.6%; Score 720.5; DB 4; Length 146;
Best Local Similarity 99.3%; Pred. No. 5.3e-70;
Matches 145; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 VPIQKVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 59
Db 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60

Qy 60 YQQLTSMPSNRVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDLSLGGVLEASGYS 119
Db 61 YQQLTSMPSNRVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDLSLGGVLEASGYS 120

Qy 120 TEVVALSRQSLQDMLWQLDLSGPC 145
Db 121 TEVVALSRQSLQDMLWQLDLSGPC 146

RESULT 13
US-10-872-198-127
Sequence 127, Application US/10872198
Publication No. US20050002897A1
GENERAL INFORMATION:
APPLICANT: Ulrich HAUPTS
APPLICANT: Andre KOLTERMANN
APPLICANT: Andreas SCHEIDIG
APPLICANT: Christian VOETSMER
APPLICANT: Ulrich Kettling
TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF
FILE REFERENCE: 04156.0002U4

APPLICANT: Ladd, David
APPLICANT: Papisov, Mikhail
TITLE OF INVENTION: PROTEIN CONJUGATES WITH A WATER-SOLUBLE BIOCOMPATIBLE, BIODEGRADABLE
TITLE OF INVENTION: POLYMER
FILE REFERENCE: A-822
CURRENT APPLICATION NUMBER: US/10/622,998
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 60/397,509
PRIOR FILING DATE: 2002-07-19
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patent in version 3.1
SEQ ID NO 1
LENGTH: 146
TYPE: PRT
ORGANISM: Homo sapiens
US-10-622-998-1

Query Match 98.6%; Score 720.5; DB 4; Length 146;
Best Local Similarity 99.3%; Pred. No. 5.3e-70;
Matches 145; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 VPIQKVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 59
Db 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60

Qy 60 YQQLTSMPSNRVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDLSLGGVLEASGYS 119
Db 61 YQQLTSMPSNRVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDLSLGGVLEASGYS 120

Qy 120 TEVVALSRQSLQDMLWQLDLSGPC 145
Db 121 TEVVALSRQSLQDMLWQLDLSGPC 146

RESULT 11
US-10-658-834A-211
Sequence 211, Application US/10658834A
Publication No. US20040132977A1
GENERAL INFORMATION:
APPLICANT: Gantier, Rene
APPLICANT: Guyon, Thierry
APPLICANT: Dristanti, Lila
APPLICANT: Vega, Manuel
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
TITLE OF INVENTION: Acid
TITLE OF INVENTION: Molecules and Related Applications
FILE REFERENCE: 38751-922
CURRENT APPLICATION NUMBER: US/10/658,834A
CURRENT FILING DATE: 2003-09-08
PRIOR APPLICATION NUMBER: 60/457,135
PRIOR FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: 60/409,898
PRIOR FILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 1306
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 211
LENGTH: 146
TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank AAA60470
DATABASE ENTRY DATE: 1995-01-13
US-10-658-834A-211

Query Match 98.6%; Score 720.5; DB 4; Length 146;
Best Local Similarity 99.3%; Pred. No. 5.3e-70;
Matches 145; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 VPIQKVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 59
Db 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60

Qy 60 YQQLTSMPSNRVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDLSLGGVLEASGYS 119
Db 61 YQQLTSMPSNRVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDLSLGGVLEASGYS 120

Qy 120 TEVVALSRQSLQDMLWQLDLSGPC 145
Db 121 TEVVALSRQSLQDMLWQLDLSGPC 146

RESULT 12
US-10-468-496-1
Sequence 1, Application US/10468496
Publication No. US20040180386A1
GENERAL INFORMATION:
APPLICANT: Carr, Francis J.
APPLICANT: Jones, Tim
APPLICANT: Williams, Stephen
APPLICANT: Hamilton, Anita
TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED
TITLE OF INVENTION: IMMUNOGENICITY
FILE REFERENCE: MER-117
CURRENT APPLICATION NUMBER: US/10/468,496
CURRENT FILING DATE: 2003-09-25
PRIOR APPLICATION NUMBER: 01103954.2
PRIOR FILING DATE: 2001-02-19
PRIOR APPLICATION NUMBER: 01105777.5
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 01106538.0
PRIOR FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 01106536.4
PRIOR FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 01107012.5
PRIOR FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 01106899.6
PRIOR FILING DATE: 2001-03-20
NUMBER OF SEQ ID NOS: 2036
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 146
TYPE: PRT
ORGANISM: Homo sapiens
US-10-468-496-1

Query Match 98.6%; Score 720.5; DB 4; Length 146;
Best Local Similarity 99.3%; Pred. No. 5.3e-70;
Matches 145; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 VPIQKVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 59
Db 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60

Qy 60 YQQLTSMPSNRVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDLSLGGVLEASGYS 119
Db 61 YQQLTSMPSNRVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDLSLGGVLEASGYS 120

Qy 120 TEVVALSRQSLQDMLWQLDLSGPC 145
Db 121 TEVVALSRQSLQDMLWQLDLSGPC 146

RESULT 13
US-10-872-198-127
Sequence 127, Application US/10872198
Publication No. US20050002897A1
GENERAL INFORMATION:
APPLICANT: Ulrich HAUPTS
APPLICANT: Andre KOLTERMANN
APPLICANT: Andreas SCHEIDIG
APPLICANT: Christian VOETSMER
APPLICANT: Ulrich Kettling
TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF
FILE REFERENCE: 04156.0002U4

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; CURRENT APPLICATION NUMBER: US/10/872,198
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,518
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 04003058
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 127
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-872,198-127

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	Query Match	98.6%	Score 720.5;	DB 5;	Length 146;
	Best Local Similarity 99.3%;	Pred. No. 5.3e-70;			
	Matches 145;	Conservative 0;	Mismatches 0;	Indels 1;	Gaps 1;
Qy	1	VPIQKVDDDKTLIKTIVTRINDISHT-SVSSKQKVTLGDFIPGLHPILTILSKMDQTLLAV	59		
Db	1	VPIQKVDDDKTLIKTIVTRINDISHTQSVSSKQKVTLGDFIPGLHPILTILSKMDQTLLAV	60		
Qy	60	YQOILTSMPSRNVIOISNDLENRLDLHLVLAFSKSCHLPWASGLETILDSLGGVLEASGYS	119		
Db	61	YQOILTSMPSRNVIOISNDLENRLDLHLVLAFSKSCHLPWASGLETILDSLGGVLEASGYS	120		
Qy	120	TEVVALSRLOGSQDMLWQLDLSPGC	145		
Db	121	TEVVALSRLOGSQDMLWQLDLSPGC	146		

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RESULT 14
US-10-623-189-1
; Sequence 1, Application US/10623189
; Publication No. US20050020496A1
; GENERAL INFORMATION:
; APPLICANT: DEPAOLI, Alex M.
; APPLICANT: ORAL, Elif Arioglu
; APPLICANT: TAYLOR, Simeon I.
; APPLICANT: GARG, Abhinav
; TITLE OF INVENTION: USE OF LEPTIN FOR TREATING HUMAN LIPOATROPHY AND METHOD OF DETERM
; TITLE OF INVENTION: PREDISPOSITION TO SAID TREATMENT
; FILE REFERENCE: 54113.8005:US02
; CURRENT APPLICATION NUMBER: US/10/623,189
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 10/279,129
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: US 60/336,394
; PRIOR FILING DATE: 2001-10-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant Leptin Human 146 (rHu-Leptin l-146)
US-10-623-189-1

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Query Match 98.6%; Score 720.5; DB 5; Length 146;
Best Local Similarity 99.3%; Pred.No. 5.3e-70;
Matches 145; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 VPIQKVDDTKLIKIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTSLKMDQTLAV 59

Db	1	VPTQKVQDDTKTLTKIVTRINDISHTSQSVSSKKQVTKGLDPI	PGLHPILTLTISKMDQTLAV	60
QY	60	YQOILTSMPGRNVIQISNDLENIRDLHLVAFSKSCHLPWASGLET	LDLSGGVLEASGYS	119
Db	61	YQOILTSMPGRNVIQISNDLENIRDLHLVAFSKSCHLPWASGLET	LDLSGGVLEASGYS	120
QY	120	TEVVALSRQGSQDMLWQLDLSPGC	145	
Db	121	TEVVALSRQGSQDMLWQLDLSPGC	146	

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RESULT 15
US-10-502-344-22
; Sequence 22, Application US/10502344
; Publication No. US20050214762A1
; GENERAL INFORMATION:
; APPLICANT: ROSS, Richard
; APPLICANT: ARTYMUK, Peter
; APPLICANT: SAYERS, Jon
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: 100042.55084US
; CURRENT APPLICATION NUMBER: US/10/502,344
; CURRENT FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: PCT/GB03/00253
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: GB 0201679.8
; PRIOR FILING DATE: 2003-01-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 22
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificial linker
US-10-502-344-22

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	Query Match	98.6%	Score 720.5;	DB 5;	Length 146;
	Best Local Similarity 99.3%;		Pred. No. 5.3e-70;		
	Matches 145;	Conservative 0;	Mismatches 0;	Indels 1;	Gaps 1;
QY	1	VPIQKVDDTKTIKTIIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTILSKMDQTUAV	59		
Db	1	VPIQKVDDTKTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTUAV	60		
QY	60	YQOILTSMPSRNVIQI.SNDLEN.RDLLHLVAFSKSCHLPWASGLETILDSLGGVLEASGY	119		
Db	61	YQOILTSMPSRNVIQI.SNDLEN.RDLLHLVAFSKSCHLPWASGLETILDSLGGVLEASGY	120		
QY	120	TEYVALSRLOGSLODMLWQLDLSPGC	145		
Db	121	TEYVALSRLOGSLODMLWQLDLSPGC	146		

Search completed: May 4, 2006, 22:02:16
Job time : 113.113 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 21:58:39 ; Search time 17.9381 Seconds
(without alignments)
374.135 Million cell updates/sec

Title: US-10-623-189-2
Perfect score: 731
Sequence: 1 VPIQKVDDTKTLKTIIVTR.....SRLOGLQDMLWQLDLSPGC 145

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:
1: /SIDSS5/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /SIDSS5/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /SIDSS5/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /SIDSS5/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
5: /SIDSS5/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
6: /SIDSS5/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
7: /SIDSS5/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
8: /SIDSS5/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
9: /SIDSS5/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
10: /SIDSS5/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
11: /SIDSS5/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
12: /SIDSS5/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	720.5	98.6	146	9	US-10-519-390-19
2	720.5	98.6	146	11	US-11-176-830-211
3	720.5	98.6	167	11	US-11-236-198-32
4	720.5	98.6	185	9	US-10-821-234-1384
5	720.5	98.6	397	11	US-11-192-219-47
6	718.5	98.3	146	11	US-11-176-830-666
7	718.5	98.3	146	11	US-11-176-830-672
8	718.5	98.3	146	11	US-11-176-830-677
9	718.5	98.3	146	11	US-11-176-830-683
10	717.5	98.2	146	11	US-11-176-830-665
11	717.5	98.2	146	11	US-11-176-830-671
12	717.5	98.2	146	11	US-11-176-830-673
13	717.5	98.2	146	11	US-11-176-830-676
14	717.5	98.2	146	11	US-11-176-830-682
15	717.5	98.2	146	11	US-11-236-198-36
16	715.5	97.9	146	11	US-11-176-830-674
17	715.5	97.9	146	11	US-11-176-830-675
18	715.5	97.9	146	11	US-11-176-830-679
19	715.5	97.9	146	11	US-11-176-830-681
20	714.5	97.7	146	11	US-11-176-830-678
21	714.5	97.7	146	11	US-11-176-830-680

22	712.5	97.5	146	11	US-11-176-830-663	Sequence 663, App
23	712.5	97.5	146	11	US-11-176-830-664	Sequence 664, App
24	712.5	97.5	146	11	US-11-176-830-667	Sequence 667, App
25	712.5	97.5	146	11	US-11-176-830-668	Sequence 668, App
26	712.5	97.5	146	11	US-11-236-198-31	Sequence 31, Appl
27	711.5	97.3	146	9	US-10-926-798-5	Sequence 5, Appli
28	707.5	96.8	146	11	US-11-176-830-670	Sequence 670, App
29	706.5	96.6	146	11	US-11-176-830-669	Sequence 669, App
30	705.5	96.5	146	11	US-11-236-198-37	Sequence 37, Appl
31	656.5	89.8	167	11	US-11-236-198-33	Sequence 33, Appl
32	612.5	83.8	167	11	US-11-236-198-28	Sequence 28, Appl
33	611.5	83.7	167	11	US-11-236-198-39	Sequence 39, Appl
34	608.5	83.2	146	11	US-11-236-198-35	Sequence 35, Appl
35	603.5	82.6	167	11	US-11-236-198-34	Sequence 34, Appl
36	597	81.7	163	11	US-11-236-198-30	Sequence 30, Appl
37	592.5	81.1	178	9	US-10-926-798-8	Sequence 8, Appli
38	589.5	80.6	167	11	US-11-236-198-38	Sequence 38, Appl
39	587.5	80.4	178	9	US-10-926-798-15	Sequence 15, Appl
40	585.5	80.1	178	9	US-10-926-798-16	Sequence 16, Appl
41	584.5	80.0	178	9	US-10-926-798-17	Sequence 17, Appl
42	583.5	79.8	146	11	US-11-236-198-29	Sequence 29, Appl
43	138.5	18.9	32	9	US-10-841-218-1	Sequence 1, Appli
44	125	17.1	26	9	US-10-841-218-2	Sequence 2, Appli
45	120	16.4	22	11	US-11-236-198-54	Sequence 54, Appl

ALIGNMENTS

RESULT 1

US-10-519-390-19
; Sequence 19, Application US/10519390
; Publication No. US2006008872A1
; GENERAL INFORMATION:
; APPLICANT: MEDEXGEN Inc.
; APPLICANT: CHUNG, Yong-Hoon
; APPLICANT: LEE, Hak-sup
; APPLICANT: YI, Ki-Wan
; APPLICANT: KIM, Jae-Youn
; APPLICANT: HEO, Youn-Hwa
; TITLE OF INVENTION: A method of improving efficacy of biological response-modifying
; TITLE OF INVENTION: proteins and the example mutants
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/519,390
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: KR10-2003-0051846
; PRIOR FILING DATE: 2003-07-26
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 19
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LPT: 41st or 92nd Phe is replaced by Val.
US-10-519-390-19

Query Match		98.6%	Score	720.5	DB	9	Length	146
Best Local Similarity		99.3%	Pred. No.	1.6e-64	Indels	1	Gaps	1
Matches		145	Conservative	0	Mismatches	0		
Qy	1	VPIQKVDDTKTLKTIIVTRINDISHT	-SVSSSKQKVTGLDFIPGLHPIILTSKMDQTLAV	59				
Db	1	VPIQKVDDTKTLKTIIVTRINDISHT	QSVSSKQKVTGLDFIPGLHPIILTSKMDQTLAV	60				
Qy	60	YQQLTSMPSRNVQISNDLENLDLHLVAFPSCHLPWASGLETLDLSGGVLEASGYS	119					
Db	61	YQQLTSMPSRNVQISNDLENLDLHLVAFPSCHLPWASGLETLDLSGGVLEASGYS	120					
Qy	120	TEVVALSRLOGLQDMLWQLDLSPGC	145					
Db	121	TEVVALSRLOGLQDMLWQLDLSPGC	146					

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RESULT 2
; Sequence 211, Application US/11176830
; Publication No. US20060020116A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
; FILE OF INVENTION: Acid Molecules and Related Applications
; FILE REFERENCE: 17109-012002 (922B)
; CURRENT APPLICATION NUMBER: US/11/176,830
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: 10/658,834
; PRIOR FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 211
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank AAA60470
; DATABASE ENTRY DATE: 1995-01-13
US-11-176-830-211

Query Match      98.6%; Score 720.5; DB 11; Length 146;
Best Local Similarity 99.3%; Pred. No. 1.6e-64;
Matches 145; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 VPIQKVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 59
Db 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

QY 60 YQQLTSMPSRNVQISNDLENLRLDLHLVLAFAKSKCHLPWASGLETLDSLGGLVLEASGYS 119
Db 61 YQQLTSMPSRNVQISNDLENLRLDLHLVLAFAKSKCHLPWASGLETLDSLGGLVLEASGYS 120

QY 120 TEVVALSRLOQSLQDMLWQDLSPGC 145
Db 121 TEVVALSRLOQSLQDMLWQDLSPGC 146

RESULT 3
US-11-236-198-32
; Sequence 32, Application US/11236198
; Publication No. US20060030530A1
; GENERAL INFORMATION:
; APPLICANT: Yen, Frances
; APPLICANT: Erickson, Mary Ruth
; APPLICANT: Fruebis, Joachim
; APPLICANT: Bihain, Bernard
; TITLE OF INVENTION: Methods Of Screening For Compounds That Modulate the
; TITLE OF INVENTION: LSR-Leptin Interaction and Their Use in the Prevention
; TITLE OF INVENTION: and Treatment of Obesity-Related Diseases
; FILE REFERENCE: 70 US2 REG
; CURRENT APPLICATION NUMBER: US/11/236,198
; CURRENT FILING DATE: 2005-09-27
; PRIOR APPLICATION NUMBER: US/09/668,558
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,506
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: Patent.pm
; SEQ ID NO 32
; LENGTH: 167
; TYPE: PRT

Query Match      98.6%; Score 720.5; DB 11; Length 146;
Best Local Similarity 99.3%; Pred. No. 1.6e-64;
Matches 145; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 VPIQKVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 59
Db 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

QY 60 YQQLTSMPSRNVQISNDLENLRLDLHLVLAFAKSKCHLPWASGLETLDSLGGLVLEASGYS 119
Db 61 YQQLTSMPSRNVQISNDLENLRLDLHLVLAFAKSKCHLPWASGLETLDSLGGLVLEASGYS 120

QY 120 TEVVALSRLOQSLQDMLWQDLSPGC 145
Db 121 TEVVALSRLOQSLQDMLWQDLSPGC 146

RESULT 4
US-10-821-234-1384
; Sequence 1384, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1384
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1384

Query Match      98.6%; Score 720.5; DB 9; Length 185;
Best Local Similarity 99.3%; Pred. No. 2.2e-64;
Matches 145; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 VPIQKVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 59
Db 40 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 99

QY 60 YQQLTSMPSRNVQISNDLENLRLDLHLVLAFAKSKCHLPWASGLETLDSLGGLVLEASGYS 119
Db 100 YQQLTSMPSRNVQISNDLENLRLDLHLVLAFAKSKCHLPWASGLETLDSLGGLVLEASGYS 159

QY 120 TEVVALSRLOQSLQDMLWQDLSPGC 145
Db 160 TEVVALSRLOQSLQDMLWQDLSPGC 185

RESULT 5
US-11-192-219-47
; Sequence 47, Application US/11192219
; Publication No. US20050272656A1
; GENERAL INFORMATION:
; APPLICANT: Matthews, William
; TITLE OF INVENTION: USES FOR WSK LIGANDS
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
```

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; ORGANISM: Homo sapiens
US-11-236-198-32

Query Match      98.6%; Score 720.5; DB 11; Length 167;
Best Local Similarity 99.3%; Pred. No. 2e-64;
Matches 145; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 VPIQKVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 59
Db 22 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 81

QY 60 YQQLTSMPSRNVQISNDLENLRLDLHLVLAFAKSKCHLPWASGLETLDSLGGLVLEASGYS 119
Db 82 YQQLTSMPSRNVQISNDLENLRLDLHLVLAFAKSKCHLPWASGLETLDSLGGLVLEASGYS 141

QY 120 TEVVALSRLOQSLQDMLWQDLSPGC 145
Db 142 TEVVALSRLOQSLQDMLWQDLSPGC 167

RESULT 4
US-10-821-234-1384
; Sequence 1384, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1384
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1384

Query Match      98.6%; Score 720.5; DB 9; Length 185;
Best Local Similarity 99.3%; Pred. No. 2.2e-64;
Matches 145; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 VPIQKVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 59
Db 40 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 99

QY 60 YQQLTSMPSRNVQISNDLENLRLDLHLVLAFAKSKCHLPWASGLETLDSLGGLVLEASGYS 119
Db 100 YQQLTSMPSRNVQISNDLENLRLDLHLVLAFAKSKCHLPWASGLETLDSLGGLVLEASGYS 159

QY 120 TEVVALSRLOQSLQDMLWQDLSPGC 145
Db 160 TEVVALSRLOQSLQDMLWQDLSPGC 185

RESULT 5
US-11-192-219-47
; Sequence 47, Application US/11192219
; Publication No. US20050272656A1
; GENERAL INFORMATION:
; APPLICANT: Matthews, William
; TITLE OF INVENTION: USES FOR WSK LIGANDS
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
```


COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/192,219
FILING DATE: 27-Jul-2005
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/667,197
FILING DATE: 20-Jun-1996
APPLICATION NUMBER: 08/585005
FILING DATE: 08-Jan-96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: P-40,378
REFERENCE/DOCKET NUMBER: P0986P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 397 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-11-192-219-47

Query Match 98.6%; Score 720.5; DB 11; Length 397;
Best Local Similarity 99.3%; Pred.No. 6.1e-64; Indels 1; Gaps 1;
Matches 145; Conservative 0; Mismatches 0;
Qy 1 VPIQKVQDDTKTLIKTIIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 59
Db 22 VPIQKVQDDTKTLIKTIIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 81
Qy 60 YQOILTSMPNRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDLSGGVLEASGYS 119
Db 82 YQOILTSMPNRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDLSGGVLEASGYS 141
Qy 120 TEVVALSRQSGSLQDMLWQLDLSGPC 145
Db 142 TEVVALSRQSGSLQDMLWQLDLSGPC 167

RESULT 6
US-11-176-830-666
Query Match 98.6%; Score 718.5; DB 11; Length 146;
Best Local Similarity 98.6%; Pred.No. 2.6e-64;
Matches 144; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
GENERAL INFORMATION:
APPLICANT: Gantier, Rene
APPLICANT: Guyon, Thierry
APPLICANT: Drittanti, Lila
APPLICANT: Vega, Manuel
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
FILE REFERENCE: 17109-012002 (922B)
CURRENT APPLICATION NUMBER: US/11/176,830
CURRENT FILING DATE: 2005-07-06
PRIOR APPLICATION NUMBER: 10/658,834
PRIOR FILING DATE: 2003-09-08
PRIOR APPLICATION NUMBER: 60/457,135
PRIOR FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: 60/409,898
PRIOR FILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 1306
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 666
LENGTH: 146

; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-176-830-666
Query Match 98.3%; Score 718.5; DB 11; Length 146;
Best Local Similarity 98.6%; Pred.No. 2.6e-64;
Matches 144; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
Qy 1 VPIQKVQDDTKTLIKTIIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 59
Db 1 VPIQKVQDDTKTLIKTIIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Qy 60 YQOILTSMPNRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDLSGGVLEASGYS 119
Db 61 YQOILTSMPNRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDLSGGVLEASGYS 120
Qy 120 TEVVALSRQSGSLQDMLWQLDLSGPC 145
Db 121 TEVVALSRQSGSLQDMLWQLDLSGPC 146

RESULT 7
US-11-176-830-672
Query Match 98.3%; Score 718.5; DB 11; Length 146;
Best Local Similarity 98.6%; Pred.No. 2.6e-64;
Matches 144; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
GENERAL INFORMATION:
APPLICANT: Gantier, Rene
APPLICANT: Guyon, Thierry
APPLICANT: Drittanti, Lila
APPLICANT: Vega, Manuel
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding
FILE REFERENCE: 17109-012002 (922B)
CURRENT APPLICATION NUMBER: US/11/176,830
CURRENT FILING DATE: 2005-07-06
PRIOR APPLICATION NUMBER: 10/658,834
PRIOR FILING DATE: 2003-09-08
PRIOR APPLICATION NUMBER: 60/457,135
PRIOR FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: 60/409,898
PRIOR FILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 1306
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 672
LENGTH: 146
TYPE: PRT
ORGANISM: Homo sapiens
US-11-176-830-672

Query Match 98.3%; Score 718.5; DB 11; Length 146;
Best Local Similarity 98.6%; Pred.No. 2.6e-64;
Matches 144; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
Qy 1 VPIQKVQDDTKTLIKTIIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 59
Db 1 VPIQKVQDDTKTLIKTIIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Qy 60 YQOILTSMPNRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDLSGGVLEASGYS 119
Db 61 YQOILTSMPNRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDLSGGVLEASGYS 120
Qy 120 TEVVALSRQSGSLQDMLWQLDLSGPC 145
Db 121 TEVVALSRQSGSLQDMLWQLDLSGPC 146
RESULT 8
US-11-176-830-677
Query Match 98.3%; Score 718.5; DB 11; Length 146;
Best Local Similarity 98.6%; Pred.No. 2.6e-64;
Matches 144; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
GENERAL INFORMATION:
APPLICANT: Gantier, Rene
APPLICANT: Guyon, Thierry

;; PRIOR APPLICATION NUMBER: 60/409,898
;; PRIOR FILING DATE: 2002-09-09
;; NUMBER OF SEQ ID NOS: 1306
;; SOFTWARE: FastSEQ for Windows Version 4.0
;; SEQ ID NO 671
;; LENGTH: 146
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-176-830-671

Query Match 98.2%; Score 717.5; DB 11; Length 146;
Best Local Similarity 98.6%; Pred. No. 3.2e-64;
Matches 144; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 VPIQKVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 59
Db 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

Qy 60 YQILTSMPNRNVIQISNDLENLDLHLVLAFSKSLPWSAGLETLDLSLGGVLEASGYS 119
Db 61 YQILTSMPNRNVIQISNDLENLDLHLVLAFSKSLPWSAGVETLDLSLGGVLEASGYS 120

Qy 120 TEVVALSRQGSLOQMLWQLDLSFGC 145
Db 121 TEVVALSRQGSLOQMLWQLDLSFGC 146

RESULT 12

US-11-176-830-673
;; Sequence 673, Application US/11176830
;; Publication No. US20060020116A1
;; GENERAL INFORMATION:
;; APPLICANT: Gantier, Rene
;; APPLICANT: Guyon, Thierry
;; APPLICANT: Drittanti, Lila
;; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
;; TITLE OF INVENTION: Acid Molecules and Related Applications
;; FILE REFERENCE: 17109-012002 (922B)
;; CURRENT APPLICATION NUMBER: US/11/176,830
;; CURRENT FILING DATE: 2005-07-06
;; PRIOR APPLICATION NUMBER: 10/658,834
;; PRIOR FILING DATE: 2003-09-08
;; PRIOR APPLICATION NUMBER: 60/457,135
;; PRIOR FILING DATE: 2003-03-21
;; PRIOR APPLICATION NUMBER: 60/409,898
;; PRIOR FILING DATE: 2002-09-09
;; NUMBER OF SEQ ID NOS: 1306
;; SOFTWARE: FastSEQ for Windows Version 4.0
;; SEQ ID NO 673
;; LENGTH: 146
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-176-830-673

Query Match 98.2%; Score 717.5; DB 11; Length 146;
Best Local Similarity 98.6%; Pred. No. 3.2e-64;
Matches 144; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 VPIQKVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 59
Db 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

Qy 60 YQILTSMPNRNVIQISNDLENLDLHLVLAFSKSLPWSAGLETLDLSLGGVLEASGYS 119
Db 61 YQILTSMPNRNVIQISNDLENLDLHLVLAFSKSLPWSAGLETLDLSLGGVLEASGYS 120

Qy 120 TEVVALSRQGSLOQMLWQLDLSFGC 145
Db 121 TEVVALSRQGSLOQMLWQLDLSFGC 146

RESULT 13

US-11-176-830-682

US-11-176-830-676
;; Sequence 676, Application US/11176830
;; Publication No. US20060020116A1
;; GENERAL INFORMATION:
;; APPLICANT: Gantier, Rene
;; APPLICANT: Guyon, Thierry
;; APPLICANT: Drittanti, Lila
;; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding N
;; TITLE OF INVENTION: Acid Molecules and Related Applications
;; FILE REFERENCE: 17109-012002 (922B)
;; CURRENT APPLICATION NUMBER: US/11/176,830
;; CURRENT FILING DATE: 2005-07-06
;; PRIOR APPLICATION NUMBER: 10/658,834
;; PRIOR FILING DATE: 2003-09-08
;; PRIOR APPLICATION NUMBER: 60/457,135
;; PRIOR FILING DATE: 2003-03-21
;; PRIOR APPLICATION NUMBER: 60/409,898
;; PRIOR FILING DATE: 2002-09-09
;; NUMBER OF SEQ ID NOS: 1306
;; SOFTWARE: FastSEQ for Windows Version 4.0
;; SEQ ID NO 676
;; LENGTH: 146
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-176-830-676

Query Match 98.2%; Score 717.5; DB 11; Length 146;
Best Local Similarity 98.6%; Pred. No. 3.2e-64;
Matches 144; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 VPIQKVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 59
Db 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

Qy 60 YQILTSMPNRNVIQISNDLENLDLHLVLAFSKSLPWSAGLETLDLSLGGVLEASGYS 119
Db 61 YQILTSMPNRNVIQISNDLENLDLHLVLAFSKSLPWSAGLETVDLSLGGVLEASGYS 120

Qy 120 TEVVALSRQGSLOQMLWQLDLSFGC 145
Db 121 TEVVALSRQGSLOQMLWQLDLSFGC 146

RESULT 14

US-11-176-830-682
;; Sequence 682, Application US/11176830
;; Publication No. US20060020116A1
;; GENERAL INFORMATION:
;; APPLICANT: Gantier, Rene
;; APPLICANT: Guyon, Thierry
;; APPLICANT: Drittanti, Lila
;; APPLICANT: Vega, Manuel
;; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding N
;; TITLE OF INVENTION: Acid Molecules and Related Applications
;; FILE REFERENCE: 17109-012002 (922B)
;; CURRENT APPLICATION NUMBER: US/11/176,830
;; CURRENT FILING DATE: 2005-07-06
;; PRIOR APPLICATION NUMBER: 10/658,834
;; PRIOR FILING DATE: 2003-09-08
;; PRIOR APPLICATION NUMBER: 60/457,135
;; PRIOR FILING DATE: 2003-03-21
;; PRIOR APPLICATION NUMBER: 60/409,898
;; PRIOR FILING DATE: 2002-09-09
;; NUMBER OF SEQ ID NOS: 1306
;; SOFTWARE: FastSEQ for Windows Version 4.0
;; SEQ ID NO 682
;; LENGTH: 146
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-176-830-682

Query Match

98.2%; Score 717.5; DB 11; Length 146;

